



D	b		241	GHEALTTPPATLISPLDSAHNTLLAPDSEKICTVOLGNSWTFGEYPTQALCPDYTW	300
O	y		240	GHEALTTPPATLISPLDSAHNTLLAPDSEKICTVOLGNSWTFGEYPTQALCPDYTW	299
D	b		301	MDLPESRALGPAAATLSPESPAGSPAMMLPGPOLYDVMDAVPARMKKEVFTLGREA	360
O	y		300	MDLPESRALGPAAATLSPESPAGSPAMMLPGPOLYDVMDAVPARMKKEVFTLGREA	359
D	b		361	ELEAVEVEIGRRDDOYEMLKRWROODPAGICAYVAALERMGDCVEDLSRLQGR	418
O	y		360	ELEAVEVEIGRRDDOYEMLKRWROODPAGICAYVAALERMGDCVEDLSRLQGR	417
<hr/>					
RESULT 2					
ID		014865	PRELIMINARY:	PRT:	426 AA.
AC		014865			
.DT		01-JAN-1998	(TREMBLrel. 05, Created)		
DT		01-JAN-1998	(TREMBLrel. 05, Last sequence update)		
DT		01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE		DEATH RECEPTOR 3 BETA.			
GN		DR3.			
OS		Homo sapiens (Human).			
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC		Eutheria; Primates; Catarrhini; Homidae; Homo.			
RP		[1]			
RN		SEQUENCE FROM N.A.			
RX		MEDLINE: 98113360.			
RA		MAZUCHA K., RIBEIRO P., CHARLOT C., RENARD N., COIFFIER B.,			
RA		SALLES G.;			
RT		"A new death receptor 3 isoform: expression in human lymphoid cell			
RT		lines and non-Hodgkin's lymphomas."			
RL		Biochem. Biophys. Res. Commun. 242:376-379(1998).			
DR		EMBL: AF026070; Acc.39556.1; .			
DR		HSSP: P19438; ITNR.			
DR		PROSITE: PS00652; TNFR_NGFR.1; 2.			
DR		PFAM: PF00531; death.1.			
DR		PFAM: PF00020; TNFR_c6; 2.			
SO		SEQUENCE 426 AA; 45950 MW; 87E00821 CRC32;			
<hr/>					
Query Match 92.1%; Score 2945; DB 4; Length 426;					
Best Local Similarity 94.1%; Pred. No. 0.00e+00;					
Matches 401; Conservative 8; Mismatches 8; Indels 9; Gaps 5;					
D	b		1	MEORRGCAAAVALLVLTGARAOGGTRSRCCADBFHKITGLFCCRGGAGHTYKAP	60
O	y		1	MEORRGCAAAVALLVLTGARAOGGTRSRCCADBFHKITGLFCCRGGAGHTYKAP	60
D	b		61	CTEPCGSTCLVCBQDFTLAWENHNHNSBCARCQAQCDQASQVALENCSAVDTRCGCKP	120
O	y		61	CTEPCGSTCLVCBQDFTLAWENHNHNSBCARCQAQCDQASQVALENCSAVDTRCGCKP	120
D	b		121	WFVECVSYSCVSSSPFYCQPCLCDGALHRHRTLCSRBDTCGLPEGYEHGDGVSCP	180
O	y		121	WFVECVSYSCVSSSPFYCQPCLCDGALHRHRTLCSRBDTCGLPEGYEHGDGVSCP	180
D	b		181	TPEPSIAGPAVGAVSAPLTSVAGRGVFWVUULLAGLVPLLGTATLYTTRHCMPKH	240
O	y		181	TS--TLGSC--E-RCA---AVGMR-QMRYVUULLAGLVPLLGTATLYTTRHCMPKH	231
D	b		241	PLYTADEAGMALTPPATLISPLDSAHTLLAPPDSEKICTVOLGNSWTFGEYPTQEA	300
O	y		232	PLYTADEAGMALTPPATLISPLDSAHTLLAPPDSEKICTVOLGNSWTFGEYPTQEA	291
D	b		301	LCPDYTWMDLPSRALGPAAATLSPESPAGSPAMMLPGPOLYDVMDAVPARMKKEV	360
O	y		292	LCPDYTWMDLPSRALGPAAATLSPESPAGSPAMMLPGPOLYDVMDAVPARMKKEV	351
D	b		361	RTTLGREAEIAVAVEVLGFPRDOOYEMLKRMROOPAGICAYVAALERMGDCVEDLS	420
O	y		352	RTTLGREAEIAVAVEVLGFPRDOOYEMLKRMROOPAGICAYVAALERMGDCVEDLS	411
D	b		421	RLQRGP 426	

0Y	412	RLRGCP	417	
RESULT	3			
ID	000280	PRELIMINARY;	PRT;	380 AA.
AC	000280;			
DT	01-JUL-1997	(TREMBLrel. 04, Created)		
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)		
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)		
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.			
OS	Homo sapiens (Human)			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97272273.			
RA	SCEATON G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,			
RA	MCMICHAEL A.J., BELL J.I.;			
RT	"LARD: a new lymphoid-specific death domain containing receptor			
RT	regulated by alternative pre-mRNA splicing";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).			
DR	EMBL: U94510; AAC51315.1; -.			
DR	HSSP: P19438; 1TRN.			
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.			
DR	PFAM: PF00531; death; 1.			
DR	PFAM: PF00020; TNFR_c6; 2.			
QY	SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;			

Query Match	Similarity	77.6%	Score 2483	DB 4	Length 380
Best Local	Similarity	90.9%	Pred. No. 0.00e+00		
Matches	37/9	Conservative	1	Mismatches 0	Indels 37
				Gaps	1
Db	1	MEQRPBGCAVAAALLLVLLGARAAGSTRSRDCDAGDFHKIKIGLFCRCRCPAGHYLKAP	60		
QY	1	MEQRPBGCAVAAALLLVLLGARAAGSTRSRDCADDFHKIKIGLFCRCRCPAGHYLKAP	60		
Db	61	CTFCRGNSTCYCQDPTFLAMENHNHNEBCARCAQACDDQASQVLALENCSAVADPRCGKPG	120		
QY	61	CTFCRGNSTCYCQDPTFLAMENHNHNEBCARCAQACDDQASQVLALENCSAVADPRCGKPG	120		
Db	121	WFEVQVQSQCWSSSPFYCQPCPLDCGALHRTLLRCRRDTCGTCPLGFEHGDGCVSCP	180		
QY	121	WFEVQVQSQCWSSSPFYCQPCPLDCGALHRTLLRCRRDTCGTCPLGFEHGDGCVSCP	180		
Db	181	TSITGSCPERRCAVCGKRO-----NEAG	203		
QY	181	TSITGSCPERRCAVCGKROFWQVYVLLAGLVPLILGATLTITTYRHCCPHKPLVTADAEAG	240		
Db	204	MEALTPPAPATHLSPLDSAHNTLLAPDSSSEKICTVIVGVNSWMTDPQYPTQALCPQVYWSW	263		
QY	241	MEALTPPAPATHLSPLDSAHNTLLAPDSSSEKICTVIVGVNSWMTDPQYPTQALCPQVYWSW	300		
Db	264	DQPSRLRGPAAPATLSPESPAGSPAMMLDGPOLYVMQAVPARMKKEVPTLGLREAE	323		
QY	301	DQPSRLRGPAAPATLSPESPAGSPAMMLDGPOLYVMQAVPARMKKEVPTLGLREAE	360		
Db	324	IEAVEVEIGFRDQOYEMLRKRWQOQDAGIGAYAAALERMGLDGCVEDLRSRLQRP	380		
QY	361	IEAVEVEIGFRDQOYEMLRKRWQOQDAGIGAYAAALERMGLDGCVEDLRSRLQRP	417		
RESULT	4	PRELIMINARY	PRT	372	AA.
ID	000279				
AC	000279				
DT	01-JUL-1997 (Tremblrel. 04, Created)				
DT	01-JUL-1997 (Tremblrel. 04, Last sequence update)				
DT	01-NOV-1999 (Tremblrel. 12, Last annotation update)				
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 8				
DE	(LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 5).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;				
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.				

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SCREATION G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,  
 RL BELL J.,  
 RU Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U94509; AAC51314.1; -;  
 DR EMBL; U94506; AAC51311.1; -;  
 DR HSSP; P19438; ITNR.  
 DR PFAM; PF00531; death; 1.  
 KW Alternative splicing.  
 SQ SEQUENCE 372 AA; 40391 MM; 430DA0D5 CRC32;

Query Match	76.68;	Score 2451;	DB 4;	Length 372;
Best Local Similarity	98.58;	Pred. No. 0.00e+00;		
Matches 321;	Conservative 2;	Mismatches 2;	Indels 1;	Gaps 1;

Db	48	CRGPA - ASQVALLNCASVADTRCGC KGMFVECOVQSQVSSSPFYQPCPLDGCALHRT	106
Qy	92	CQADEBQASQVALLNCASVADTRCGC KGMFVECOVQSQVSSSPFYQPCPLDGCALHRT	151
Db	107	RLCSRDPDTCGTC LPGFTEHGDGCVSCPSTLGSCEPCAAYCGMRQMTVOYLLAGLV	166
Qy	152	RLCSRDPDTCGTC LPGFTEHGDGCVSCPSTLGSCEPCAAYCGMRQMTVOYLLAGLV	211
Db	167	VPLLIGATLTYTRHCPMHPRLVYTADEAGMEALTPPATHLSP LDSNHTLLAPPDSEKI	226
Qy	212	VPLLIGATLTYTRHCPMHPRLVYTADEAGMEALTPPATHLSP LDSNHTLLAPPDSEKI	271
Db	227	CTVOLVGNSTPGYRPEFOEALCPQVYTWSDQLSRALGPAAPTLSPESPAGSPAMMLOP	286
Qy	272	CTVOLVGNSTPGYRPEFOEALCPQVYTWSDQLSRALGPAAPTLSPESPAGSPAMMLOP	331
Db	287	GPQLYDVMDAIPARRMKFEVYTLRLAEALAEAVEVEIGRFDQOYEWLKRMRQOPAGLS	346
Qy	332	GPQLYDVMDAIPARRMKFEVYTLRLAEALAEAVEVEIGRFDQOYEWLKRMRQOPAGLS	391
Db	347	AVYAAALERMGLDGCVEDLRSRLQGP	372
Qy	392	AVYAAALERMGLDGCVEDLRSRLQGP	417

RESULT	5	PRELIMINARY;	PRT;	253 AA.
ID	000276			
AC	000276;			
DT	01-JUL-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)			
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
NC	Eutheria; Primates; Catarrhini; Homiinae; Homo.			
RC	11			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97272273.			
RA	SCREATOR G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,			
RA	MCMICHAEL A.J., BELL J.I.;			
RT	"LARD: a new lymphoid-specific death domain containing receptor			
RT	regulated by alternative pre-mRNA splicing.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).			
DR	HML: U94503; AAC51308.1; .			
DR	HSSP: P19438; 1TNR			
DR	PROSITE: PS00652; TNFR_NGFR_1: 2.			
QO	PRAM; P00020; TNFR_c6: 2.			
QO	SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;			

Query Match	49.3%	Score 1577	DB 4:	length 253;
Best Local Similarity	99.0%	Pred. No.	0.00+00;	
Matches	200;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
Db	1 MEORPRCAAAVAAALLLVLLGARGOGGTRSPRCACADPHKKIGLFCRCRGCPAGHYTKAP	60		
	1 MEORPRCAAAVAAALLLVLLGARGOGGTRSPRCACADPHKKIGLFCRCRGCPAGHYTKAP	60		

Db	61	CTEPGNTCTVCPDPTFLAENHNHNEBCARCAQCADBDQAQVALAENCSAADTRCGCKPG	120
QY	61	CTEPGNTCTVCPDPTFLAENHNHNEBCARCAQCADBDQAQVALAENCSAADTRCGCKPG	120
Db	121	MFVECVQSVQVSSSPFYCQPLDGLGALHRRHTRLLCSRRDIDCGTCLPGFYEHHDGCVSCP	180
QY	121	MFVECVQSVQVSSSPFYCQPLDGLGALHRRHTRLLCSRRDIDCGTCLPGFYEHHDGCVSCP	180
Db	181	TSTLGSCEPERCAAVCGMRQRM 202	
QY	181	TSTLGSCEPERCAAVCGMRQRM 202	

RESULT	6		
ID	014866	PRELIMINARY;	PRT; 277 AA.
	014866		

DT 01-JAN-1998 (TREMblrel. 05 Created)  
DT 01-JAN-1998 (TREMblrel. 05, last sequence update)  
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)  
DE SOLUBLE DEATH RECEPTOR 3 BETA.  
GN DR3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Outtheria; Primates; Catarrhini; Hominiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA WAROCCHA K., RIBETRO P., RENARD N., CHARLOT C., COIFFIER B.,  
RA SALES G.;  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026071; AAB82288.1; -  
DR HSSP; P19438; 1TNR.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PFAM; PF00020; TNFR\_66; 2.  
SQ SEQUENCE 277 AA; 2911 MW; 06E165C7 CRC32;

Query Match	44.5%;	Score 1423;	DB 4;	Length 277;
Best Local Similarity	99.5%;	Pred. No. 2.10e-289;		
Matches	181;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

[illegible]

RESULT	7		
ID	000278;	PRELIMINARY;	PRT; 234 AA.
AC	000278;		
DT	01-JUL-1997 (TREMBLrel. 04, Created)		
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)		
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 7.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE; 97272273.		
RX	SCHEATON G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,		
RA	MCMICHAEL A.J., BELL J.I.;		
RT	"LARD: a new lymphoid-specific death domain containing receptor		
RT	regulated by alternative pre-mRNA splicing.";		

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RL  PROC. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
DR  EMBL; U94508; AAC51313.1; -.
DR  PFIAM; PF00531; death; 1.
SQ  SEQUENCE 234 AA; 25373 MW; 272FD3C9 CRC32;

Query Match
Best Local Similarity 100.0%; Pred. No. 1,37e-267;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db  53 ADEGMALPPPAHTSLDASHTLAPDPSSEKICIVOLGNSWTPGPTOTALCPQ 112
    |||||||
QY  236 ADEGMALPPPAHTSLDASHTLAPDPSSEKICIVOLGNSWTPGPTOTALCPQ 295
    |||||||
Db  113 VTWGMDLPSPALPAAAPTLSPESPAGSPAMMLQPGFOLYDMDAVPARMKKEFVRTLG 172
    |||||||
QY  296 VTWGMDLPSPALPAAAPTLSPESPAGSPAMMLQPGFOLYDMDAVPARMKKEFVRTLG 355
    |||||||
Db  173 LREAIEAVEVEIGFRFOOYEMLKRMOQOPAGIGAVYALERGLDGCVEDLSRIOR 232
    |||||||
QY  356 LREAIEAVEVEIGFRFOOYEMLKRMOQOPAGIGAVYALERGLDGCVEDLSRIOR 415
    |||||||
Db  233 GP 234
    ||
QY  416 GP 417

RESULT 8
ID  000277; PRELIMINARY; PRT; 126 AA.
AC  000277;
DT  01-JUL-1997 (Tremblrel. 04, Created)
DT  01-JUL-1997 (Tremblrel. 04, Last sequence update)
DE  01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE  LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 6.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    OC  Eutheria; Primates; Catarrhini; Homiidae; Homo.
    (1)
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 97272273.
RA  SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,
    RA  MICHAEL A.J., BELL J.I.;
    RT  "LARD: a new lymphoid-specific death domain containing receptor
    RT  regulated by alternative pre-mRNA splicing."
    RT  Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RL  EMBL; U94507; AAC51312.1; -.
SQ  SEQUENCE 126 AA; 13349 MW; B4B4051A CRC32;

Query Match
Best Local Similarity 92.2%; Pred. No. 4.18e-72;
Matches 59; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Db  48 CRGCPA-ASOVALENCASAVADTRCGCKRGWFEQOVSCVSSSPFYCOPCLDGLAHRT 106
    |||||||
QY  92 CQACDEQASOVALENCASAVADTRCGCKRGWFEQOVSCVSSSPFYCOPCLDGLAHRT 151
    |||||||
Db  107 RLIC 110
    |||||
QY  152 RLIC 155

RESULT 9
ID  019131; PRELIMINARY; PRT; 471 AA.
AC  019131;
DT  01-JAN-1998 (Tremblrel. 05, Created)
DT  01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE  01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE  TUMOR NECROSIS FACTOR-RECEPTOR I.
OS  TNF-RI.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    OC  Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
    OC  Bovinae; Bos.
    (1)
RN  [1]

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RP  SEQUENCE FROM N.A.
RC  TISSUE-AORTA;
RA  LEE E.-K., TAYLOR M.J., KEHRLI M.E.;
RL  Submitted (Feb-1997) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U90937; AAB65143.1; -.
DR  HSSP; P19438; 1TNR.
DR  PROSITE; PS00652; TNFR_NGFR_1; 3.
DR  PFIAM; PF00531; death; 1.
DR  PFIAM; PF00020; TNFR_C6; 3.
SQ  SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;

Query Match
Best Local Similarity 30.0%; Pred. No. 3.50e-31;
Matches 128; Conservative 79; Mismatches 169; Indels 51; Gaps 34;

Db  40 RESPCP-QGKYNHPONSTICCTCHGTYLINDCPGPRDTCRVCAFGTYTLENHRLR 98
    |||||
QY  29 RSRCPCAGDF-HKKYGLFCCRCPCAGHYLKAPCTPCGNSSTLCVCPDFTLWENHNS 87
    |||||
Db  99 -CLSCRCDEMPQVEISPCVVDRTVCGCRKQRYREY-GE-TGPRCLNCSLCPN-GTY 154
    |||||
QY  88 ECARGCQACDEQASOVALENCASAVADTRCGCKRGWFEQOVSCVSSSPFYCOPCLDGL 147
    |||||
Db  155 NIPCO--ERDPTIC-HCHMGFFLKAKCISCHDCKNKECEKLPPTSTGKSDPPTT 210
    |||||
QY  148 HRHRLCRRDPTDCTGLPGFYEHGDCVSCPTSLGSCPERCA-VC-GW-RQHFVQ 204
    |||||
Db  211 VLLPLVYFGLCLASAVYLACRYWRKPKLYSIICGSLTVKGEDELLVAPGFNP 270
    |||||
QY  205 VLLAGLVV-PL-LIG-ATLTYYR-HCWPRK--PLV---T-ADEGMALTP-P-- 249
    |||||
Db  271 TWICSSPTSSPVSIPYISCDNSFGAVASPSSTAPPLKAGTLPCPPASTHLCTP 330
    |||||
QY  250 THL--SPDASHTLAP--DSSEK--ICTVOLGNSWTPGPTOTALC-POYTSW-DQ 302
    |||||
Db  331 GPPASTHLCTPPASTHLCTPVQKWEASAPSDQLADAPATLYAVYDGVPPSSMKEL 390
    |||||
QY  303 -LPSRA-L--GPAAPTL-SP---ESPA-GSPAMMLQPGP-LYDMDAVPARMKKE 350
    |||||
Db  391 VRLIGSEHEIRLEENRHLREAOYSMLAMRRTPREATLELLGRLRMDLGL 450
    |||||
QY  351 VRLIGSEHEIRLEAVEIQR-FRDOOYEMLKRMOQOP--AGLAVYALERGLDGC 406
    |||||
Db  451 ENIEEAL 457
    |||||
QY  407 EDLRSRL 413

RESULT 10
ID  09Y606; PRELIMINARY; PRT; 616 AA.
AC  09Y606;
DT  01-NOV-1999 (Tremblrel. 12, Created)
DT  01-NOV-1999 (Tremblrel. 12, Last sequence update)
DE  01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE  RECEPTOR ACTIVATOR OF NUCLEAR FACTOR-KAPPA B.
OS  RANK.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
    OC  Eutheria; Primates; Catarrhini; Homiidae; Homo.
    (1)
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 98032977.
RA  ANDERSON D.M., MARASKOVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,
    RA  TOMETSKO M.E., ROUX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,
    RA  GALIBERT L.;
    RT  "A homologue of the TNF receptor and its ligand enhance T-cell growth
    RT  and dendritic-cell function."
    RT  Nature 390:175-179(1997).
RL  EMBL; AF018253; AAB86809.1; -.
KW  Receptor.
SQ  SEQUENCE 616 AA; 66033 MW; 6AF398F8 CRC32;

Query Match
7.1%; Score 228; DB 4; Length 616;

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Seq	SEQUENCE	189 AA;	21324 MW;	24A93EBF CRC32;
S0	Query Match	6.6%;	Score 210;	DB 6;
	Best Local Similarity	31.8%;	Pred. No. 4,16e-19;	Length 189;
	Matches	47;	Conservative	23; Mismatches 66; Indels 12; Gaps 8;
D0	44 CPQKYLHPDDSDICCTKCKHGYLLYNDCEPRLDITCCRECENGSTFPASENHLR-QCLSC	102		
Q0	35 CA-GDF-HKKIGLPCRCRCAPGHLYLKAPCTEPCGNSICLYCPDPTFLAMNHNHSECARC	92		
D0	103 SKCRENNQVEILSPCTQYLRDIFVGCGRAN--QYEFYV--SETTLQCNNSCLC--LNTQY	155		
Q0	93 QACDQASQVVALENCSSAVADQCKRQWFEVCOVSSSPFYCOPCLDCGALHRTNR	152		
D0	156 ISCOEKONTIC-TCHAGFLFLEHRCVSC	182		
Q0	153 LLC-SRRDTCGTCLPGFYEHDGCVSC	179		
RESULT	13			
ID	035305	PRELIMINARY;	PRT;	625 AA.
AC	035305;			
DT	01-JAN-1998 (Tremblrel, 05, Created)			
DT	01-JAN-1998 (Tremblrel, 05, Last sequence update)			
DT	01-NOV-1999 (Tremblrel, 12, Last annotation update)			
DE	RECEPTOR ACTIVATOR OF NF-KAPPA B (RANK).			
GN	TNFRSF1A OR RANK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-LIVER EPITHELIUM;			
RX	MEDLINE: 98032977.			
RA	ANDERSON D.M., MARASKOVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,			
RA	TOMETSKO M.E., ROUX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,			
RA	GALIBERT L.;			
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth			
RT	and dendritic-cell function."			
RL	Nature 390:175-179(1997).			
DR	EMBL: AF019046; AAB86810.1; -.			
DR	HSSP: P25942; ICDP.			
DR	MGI: 1314891; Tnf1sfla.			
DR	PFAM: PF00020; TNFR_c6; 3.			
S0	SEQUENCE 625 AA; 66621 MW; A01B6C5B CRC32;			
	Query Match	6.6%;	Score 212;	DB 11;
	Best Local Similarity	32.0%;	Pred. No. 1.74e-19;	Length 625;
	Matches	56;	Conservative	30; Mismatches 69; Indels 20; Gaps 17;
D0	1 MAPARRRRRLQAPLALCVLLPVLDTQTPRCPTDERTYEN-LGR-CSSRCEPGLYS	58		
Q0	1 MEQRRGCAAAVALDL-L-VELGARAQGTSPRCDCAGDFHKKIGLFCRCGAPAGHYLK	58		
D0	59 SKCT-PTSDVSLCPGDEYLDTP-NEEDK-CLLHKVCDAKALVADPQNHAPRRAC	115		
Q0	59 APCETPCGNSICLYCPDPTFL-AMENHNHNSCASCQACDQASQVVALENCSSAVADTRCGC	117		
D0	116 TAGHWNSDCE-C-CRRNTE--CAGP--GA-Q-HPLQ-LNK-DYVCTPCLLGF	160		
Q0	118 KPG-WFEVCOVSSCVSSSPFYCOPCLDCGALHRTNRLLCSRRDTCGTCLPGFY	170		
RESULT	14			
ID	095185	PRELIMINARY;	PRT;	189 AA.
AC	095185;			
DT	01-FEB-1997 (Tremblrel, 02, Created)			
DT	01-JUN-1998 (Tremblrel, 06, Last sequence update)			
DT	01-NOV-1999 (Tremblrel, 12, Last annotation update)			
DE	TUMOUR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).			
GN	TNFR-1.			
OS	Felis silvestris catus (Cat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			

OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.

RN [1]

RP SEQUENCE FROM N.A.

RA DUTHIE S., NASIR L., ECKERSALL P.D.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: U72344; AAB95089.1; -.

DR HSSP: P19438; 1EXT.

DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.

DR PFAM: PF00020; TNFR\_C6; 3.

FT NON TER 189

SO SEQUENCE 189 AA; 21420 MW; 687732D2 CRC32;

Query Match

6.4%; Score 206; DB 6; Length 189;

Best Local Similarity 31.8%; Pred. No. 2.35e-18;

Matches 49; Conservative 24; Mismatches 67; Indels 14; Gaps 11;

Db 40 RAIPCP-OGKXIHPODNSICCKHKGTLYNDCEGPGIDTDCRENGTFTASENYLR- 97

QY 29 RSPRCDCAGDF-HKKIGLFCRCRCPAGHYLKAPECTPCGNSSTCLVCPDPTFLAMENHNS 87

Db 98 QCLSCSKCKEMGYEISPCFYVRYDTCGCRK---N-QY-RYVWSETHF-Q-CLNCSIC 149

QY 88 ECARQQAQDEQASVALENCASAVADTRCGCKPGWFEQVSOQVSSSPFYCQPCLDGCA- 146

Db 150 LNGTVQISCKETQNTVC-TCHAGFLRGNECVSC 182

QY 147 LHRHTRLCS--RRDTCGCTCLPGFYEHDGCVSC 179

RESULT 15

ID 09XS60 PRELIMINARY; PRT; 263 AA.

AC 09XS60;

DT 01-NOV-1999 (TREMblrel. 12, Created)

DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)

DE FAS ANTIGEN SPLICED VARIANT.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.

RN [1]

RP SEQUENCE FROM N.A.

RA ISONO T., TANBE Y., NAGANO Y., SETO A.;

RT "Splicing and allelic variation in the rabbit Fas antigen gene.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AB021297; BAA78429.1; -.

SO SEQUENCE 263 AA; 30374 MW; 43BF129F CRC32;

Query Match

6.3%; Score 202; DB 6; Length 263;

Best Local Similarity 34.0%; Pred. No. 1.31e-17;

Matches 32; Conservative 19; Mismatches 37; Indels 6; Gaps 5;

Db 41 GNFCQQLCPPTGKKKADCTSNKGKPCDCEPCEGEYTD-KSHFSSKCRCSLGDGEHGLE 99

QY 44 GLFCRCRCPAGHYLKAPECTPCGNSSTCLVCPDPTFLAMENHNSCARQACD-EQASQ 101

Db 100 VETD-CTTIQNTKCRCKSNF--CNALKEHCDP 130

QY 102 VALENCASAVADTRCGCKPGWFEQVSOQVSSSP 135

Search completed: Tue Jul 25 22:23:58 2000  
Job time : 37 secs.

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 06:03:21 ; Search time 1177.05 Seconds  
(without alignments)  
1901.371 Million cell updates/sec

Title: US-09-314-889-3  
Perfect score: 1254  
Sequence: 1 ATGGAGCAGCGCGCGCGGGG.....GCCTGCACCGCGCGCGCTGA 1254

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 892348106 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl: \*  
1: gb\_ba1: \*  
2: gb\_ba2: \*  
3: gb\_om: \*  
4: gb\_ov: \*  
5: gb\_pat: \*  
6: gb\_ph: \*  
7: gb\_pl1: \*  
8: gb\_pl2: \*  
9: gb\_pl1: \*  
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11: gb\_pl3: \*  
12: gb\_ro: \*  
13: gb\_sts: \*  
14: gb\_sy: \*  
15: gb\_un: \*  
16: em\_fun: \*  
17: em\_hum1: \*  
18: em\_hum2: \*  
19: em\_in: \*  
20: em\_om: \*  
21: em\_or: \*  
22: em\_ov: \*  
23: em\_pat: \*  
24: em\_ph: \*  
25: em\_pl: \*  
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57: gb\_htg14: \*  
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66: em\_hum6: \*  
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76: gb\_htg27: \*  
77: gb\_htg28: \*  
78: gb\_htg29: \*  
79: gb\_htg30: \*  
80: gb\_htg31: \*  
81: gb\_v11: \*  
82: gb\_v12: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1254	100.0	1254	11	HSU72763
2	1254	100.0	1254	11	HSU78029
3	1254	100.0	1254	11	HSU94501
4	1254	100.0	1634	11	HSU74611
5	1241	99.0	1257	11	HSU94502
6	1234.8	98.5	1528	11	HSU83597
7	1233.8	98.4	1557	11	HSU75380
8	1197.4	95.5	1669	11	AF026070
9	1143	91.1	1355	11	HSU94503
10	1133.4	90.4	1743	9	HSWSL1
11	1132	90.3	1198	11	HSU94504
12	1103.4	88.0	1763	11	AF026071
13	1022	81.5	1143	11	HSU94510
14	974	77.7	1119	11	HSU94509
15	910	72.6	1087	11	HSU94505
16	630	50.2	952	11	HSU94506
17	547.8	43.7	705	11	HSU94508
18	535.4	42.7	809	11	HSU94512
19	527.4	42.1	816	11	HSU83598
20	526.4	42.0	808	11	HSU73381
21	510.4	40.7	838	11	HSU94507
22	342.2	27.3	651	11	HSU83599
23	331.4	26.4	121345	40	AL158217
24	217.4	17.3	18015	12	AF134858

C	25	163.6	13.0	523	13	G37503
	26	134.8	10.7	665	11	HS083600
	27	85.4	6.8	281	11	HS094511
	28	74.2	5.9	2440	3	BT090937
	29	72.8	5.8	2004	3	BT090934
	30	66.8	5.3	1368	5	A29098
	31	66.8	5.3	2061	5	A20255
	32	66.8	5.3	2062	5	A15322
	33	66.8	5.3	2062	5	I43805
	34	66.8	5.3	2087	9	HMTNFR
	35	66.8	5.3	2111	5	A26412
	36	66.8	5.3	2111	9	HMTNFRB
	37	66.8	5.3	2112	9	HMTNFR
	38	66.8	5.3	2161	9	HSTNFRIC
	39	66.8	5.3	2175	5	A43873
	40	66.8	5.3	2175	5	A78738
	41	66.8	5.3	2175	5	AR041076
	42	66.8	5.3	2175	5	164751
	43	66.8	5.3	2176	5	A19907
	44	66.8	5.3	2254	10	UMTNFR10S3
	45	66.8	5.3	188488	39	AC006057
						AC006057 Homo sapi
						G37503 SHGC-57889
						083600 Human death
						094511 Human lymph
						090937 Bos taurus
						019994 Sus scrofa
						A29098 Synthetic D
						A20255 55kd recept
						A21522 TNF alpha 9
						I43805 Sequence 24
						M33294 Human tumor
						A26412 CDNA for (5
						M58286 Homo sapien
						M63121 Human tumor
						X55313 H.sapiens T
						A43873 Sequence 1
						A78738 Sequence 7
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						164751 Sequence 1
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						M75866 Human tumor
						AC006057 Homo sapi

## ALIGNMENTS

Query Match	100.0%	Score 1254	DB 11	Length 1254
Best Local Similarity	100.0%	Pred. No. 2.4e-204		
Matches 1254	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	ATGAGACAGCGCCCGGGGCTGCCGCGCGGCGCGCGCGCGCTCTCTCGGTGTGCTGCG	60	
Db	1	ATGAGACAGCGCGCCCGGGGCTGCCGCGCGGCGGTGGCGCGCGCGCTCTCTCGGTGTGCTGCG	60	
QY	61	GGGGCCCCGGCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACATTCCAC	120	
Db	61	GGGGCCCCGGCCAGGGCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTACATTCCAC	120	
QY	121	AAGAGATTGGTCTCTTTTGTGCAGAGGCTCCCAAGCGGGGCACTACTGAAAGGCCCT	180	
Db	121	AAGAGATTGGTCTCTTTTGTGCAGAGGCTCCCAAGCGGGGCACTACTGAAAGGCCCT	180	
QY	181	TGCACGGAGCCCTGGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACTTCTTGGCC	240	
Db	181	TGCACGGAGCCCTGGCGGCACTCCACCTGCTGTGTGTGCCCAAGACACTTCTTGGCC	240	

RESULT	1
LOCUS	HSU72763
DEFINITION	Human death receptor 3 (DR3) mRNA, complete cds.
ACCESSION	U72763
VERSION	U72763.1
KEYWORDS	GI:1669511
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1254)
TITLE	Chinnaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M., Duan, P.R., Xing, L., Gentz, R., Ni, J., and Dixit, V.M., Signal transduction by DR3, a death domain-containing receptor related to TNFR-1 and CD95
JOURNAL	Science 274 (5289), 990-992 (1996)
MEDLINE	97081063
REFERENCE	2 (bases 1 to 1254)
AUTHORS	Chinnaiyan, A.M., O'Rourke, K., Yu, G.-L., Lyons, R.H., Garg, M., Duan, P.R., Xing, L., Gentz, R., Ni, J., and Dixit, V.M., Direct Submission
TITLE	Submitted (29-sep-1996) Pathology, University of Michigan Medical School, 1301 Catherine St., Box 0602, Ann Arbor, MI 48109, USA
JOURNAL	
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BASE COUNT	201 a 420 c 407 g 226 t
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Db	301	CAGGTGGCGCTGGAGAACTTTGACGAGTGGCCGACACCCCGCTGTGGCTGTAAAGCCAGGC	360
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Db	361	TGGTTTGTGGAGTGGCCAGGTCAAGCAATGTGTACAGATTCAACCTTGTACTGTCCAACCA	420
Qy	421	TGCTTAAGTATGCGGGGGCCCTGTGCACCGGCACACAGGCTACTGTGTTCGCCAGAGATCT	480
Db	421	TGCTTAAGTATGCGGGGGCCCTGTGCACCGGCACACAGGCTACTGTGTTCGCCAGAGATCT	480
Qy	481	GACTGTGGAGACTGCGCTGCGCTGTCTATGAACATGAGGATGAGTGCGTGCTGCGCCCC	540
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Qy	541	ACGAGACACCCTGGGGAGCTGTCCAGAGCGGTGTGCGCTGTGTGGCTGTGAGGACATG	600
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Qy	601	TTTCTGGTCCAGATGCTCTCTGTGCGCTTGTGTGTCCCTCTCTGTTGGGGCACCTG	660
Db	601	TTTCTGGTCCAGATGCTCTCTGTGCGCTTGTGTGTCCCTCTCTGTTGGGGCACCTG	660
Qy	661	ACCTACACATACCGCCACTCTGTGGCTTCACAAAGCCCTGGTTACAGACATAAACTGG	720
Db	661	ACCTACACATACCGCCACTCTGTGGCTTCACAAAGCCCTGGTTACAGATAAACTGG	720
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Db	721	ATGAGAGCTCTGAACCCACCCACCGGCGCACCATCTGTCAACCTTGGAGAGCGCCACAC	780
Qy	781	CTTCTACACCTCTGTACACAGATGAGAAATGTGCACCGCTCAAGTTGGTGGTTAAACG	840
Db	781	CTTCTACACCTCTGTACACAGATGAGAAATGTGCACCGCTCAAGTTGGTGGTTAAACG	840
Qy	841	TGGACCCCTGGCTACCCCGAGACCCAGAGGGCGCTGTGCCGAGGTGACATAGTTCGG	900
Db	841	TGGACCCCTGGCTACCCCGAGACCCAGAGGGCGCTGTGCCGAGGTGACATAGTTCGG	900
Qy	901	GACCACTTGGCCACAGAGCTCTTTGGCCCGCGTGTGTGGCCCACACTCTCGCCAGAGTCC	960
Db	901	GACCACTTGGCCACAGAGCTCTTTGGCCCGCGTGTGTGGCCCACACTCTCGCCAGAGTCC	960
Qy	961	CCACCCGAGCTGGCCAGCATGATGTCTGACAGCGGGGCCCGACGCTTACAGAGTATGAC	1020
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OY 1021 GGGGTCACAGCGGCGCTGGAAGAGTTCGCGCAGCGTGGGGTGGCGGAGAG 1080  
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DB 1021 GCGGTCCAGCGGGGCTGGGAAGAGTTCGCGCAGCGTGGGGTGGCGGAGAG 1080  
OY 1081 ATCGAAGCGGTGGAGTGGAGATCGCGCCCTTCGAGACAGCATGATGCTCAAG 1140  
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DB 1081 ATCGAAGCGGTGGAGTGGAGATCGCGCCCTTCGAGACAGCATGATGCTCAAG 1140  
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DB 1141 CGCTGGCGCAGCAGCGCGCGGCGCTCGGAGCGCTTACCGGGCCCTGGAGCGCATG 1200  
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DB 1201 GGGCTGGAGCGCTGGTGGAGAGACTTGGCAGCGCGCTGGAGCGCGCGCATG 1254

RESULT 2  
HSU78029 1254 bp mRNA PRI 15-JAN-1997  
LOCUS Human apoptosis inducing receptor AIR mRNA, complete cds.  
DEFINITION U78029.1 GI:1778763  
ACCESSION  
VERSION U78029.1 GI:1778763  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Degli-Esposti, M.A., and Goodwin, R.G.  
TITLE Degli-Esposti, M.A., Din, W.S., Cosman, D., Smith, C.A. and Goodwin, R.G.  
AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis  
unpublished  
2 (bases 1 to 1254)  
Degli-Esposti, M.A. and Goodwin, R.G.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51  
University Street, Seattle, WA 98101, USA

FEATURES  
source  
Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 2.4e-204;  
Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GGGGCGCGGCGGCGGCGGCGCTGTAGCCCGCAGGTGTGACTGTGCGGTGCTTCCAC 120  
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DB 541 ACAGGACACCTGGGGAGACTGTGCAGAGCGGTGCGCTGCTGCTGCTGCTGCTGCTG 600  
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DEFINITION  
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VERSION  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 1254)  
Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.  
LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing  
Proc Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)  
97272273  
2 (bases 1 to 1254)  
Screation,G.R.  
Direct Submission  
TITLE Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK

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DEFINITION Human Apo-3 mRNA, complete cds.
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VERSION U74611.1 GI:1763292
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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1 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Apo-3, a new member of the tumor necrosis factor receptor family,
contains a death domain and activates apoptosis and NF-kB
Curr. Biol. (1996) In press
JOURNAL
2 (bases 1 to 1634)
Marsters,S.A., Sheridan,J.P., Donahue,C.J., Pitti,R.M., Gray,C.L.,
Goddard,A.D., Bauer,K.D. and Ashkenazi,A.
Direct Submission
TITLE Submitted (15-OCT-1996) Molecular Oncology, Genentech, 460 Pt. San
JOURNML Bruno Blvd., South San Francisco, CA 94080, USA
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DEFINITION Human lymphocyte associated receptor of death 1b mRNA,
ACCESSION alternatively spliced, complete cds.
VERSION U94502.1 GI:2071950
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
1 (bases 1 to 1528)  
Chaudhary, P.M. and Hood, L.E.  
Submitted (03-JAN-1997) Molecular Biotechnology, University of  
Washington, 1705 NE Pacific Street, HSB-K360, Seattle, WA 98195,  
USA

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VERSION U75380.1 GI:1695924  
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ORGANISM Homo sapiens  
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AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,  
Thome, M., Bernand, T., Hahne, M., Schrotter, M., Becker, K., Wilson, A.,  
Frensch, L.E., Browning, J.U., Macdonald, R. and Tschopp, J.  
TRAMP, a novel apoptosis-mediating receptor with sequence homology  
to tumor necrosis factor receptor 1 and Fas (Apo-1/CD95)  
JOURNAL Immunity 6 (1), 79-88 (1997)  
MEDLINE 97205335

REFERENCE 2 (bases 1 to 1557)  
 AUTHORS Bodmer, J.L., Burns, K., Schneider, P., Hofmann, R., Steiner, V.,  
 Thome, M., Bormand, T., Hahne, M., Schroter, M., Wilson, A.,  
 French, L.E., Browning, J.L., Macdonald, R. and Tschopp, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-OCT-1996) Institute of Biochemistry, University of  
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 Switzerland

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 Db 9 GGGCTGGCGCGGTTGGGCGGCGCTCTCTCTGTTGCTGGGGGCGCGGCGCGGCGG 68

OY 78 CGGCACTGTAAGCCCGAGGCTGTAAGCTGCGGCTGACTTCCAAAGAAATTGTTCTGTT 137  
 Db 69 CGGCACTGTAAGCCCGAGGCTGTAAGCTGCGGCTGACTTCCAAAGAAATTGTTCTGTT 128

OY 138 TTGTTGCAAGAGGCTGCCAGCGGGGCACTTACCTGAAGGCCCTTCCAGGAGCCTCGCG 197  
 Db 129 TTGTTGCAAGAGGCTGCCAGCGGGGCACTTACCTGAAGGCCCTTCCAGGAGCCTCGCG 188

OY 198 CAATCCACGCTGCTGTTGTTGCCCAAGACACCTTTGGCTGGGGAACACACCATTA 257  
 Db 189 CAATCCACGCTGCTGTTGTTGCCCAAGACACCTTTGGCTGGGGAACACACCATTA 248

OY 258 TTCTGAATGTCGCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTTGGCCCTGAGAA 317  
 Db 249 TTCTGAATGTCGCCGCTGCCAGGCTGTGATGAGCAGGCTCCAGGTTGGCCCTGAGAA 308

OY 318 CTGTTGACAGATGGCGGACACCCGCTGTGGCTGTAAAGCAGGCTGTTTGTGAATGCCA 377  
 Db 309 CTGTTGACAGATGGCGGACACCCGCTGTGGCTGTAAAGCAGGCTGTTTGTGAATGCCA 368

OY 378 GGTAGCAATGTTGACAGATGTCACCTTCTACTGCAACCATGCTTAAGATGCGGGGCG 437  
 Db 369 GGTAGCAATGTTGACAGATGTCACCTTCTACTGCAACCATGCTTAAGATGCGGGGCG 428

OY 438 CTTGACACCGCACACAGCGCTACTCTGTTCCCGAGAGATAGCTGAGTGGAGCTGCGCT 497  
 Db 429 CTTGACACCGCACACAGCGCTACTCTGTTCCCGAGAGATAGCTGAGTGGAGCTGCGCT 488

OY 498 GCTGGCTTCTATGAACATGGCGATGGCTGGCTGCTGCGCCACAGAGCACCCTGGGAG 557  
 Db 11 GCTGGCTTCTATGAACATGGCGATGGCTGGCTGCTGCGCCACAGAGCACCCTGGGAG 548

Db 489 GCTGGCTTCTATGAACATGGCGATGGCTGGCTGCTGCGCCACAGAGCACCCTGGGAG 548  
 OY 558 CTGTCCAGAGCGGTGGCGGCTGTCTGTGGCTGGAGGAGATGTTGTGGGTCCAGGTCGT 617  
 Db 549 CTGTCCAGAGCGGTGGCGGCTGTCTGTGGCTGGAGGAGATGTTGTGGGTCCAGGTCGT 608  
 OY 618 CTTGGCTGCTGTTGGTGGTCCCTCTCTGCTTGGGGGCGACCTGACCTACATACCGCA 677  
 Db 609 CTTGGCTGCTGTTGGTGGTCCCTCTCTGCTTGGGGGCGACCTGACCTACATACCGCA 668  
 OY 678 CTGCTGGCTTCCAGAGCCCTGTTACTGACATGAAGCTGGATGAGGCTGTGACCC 737  
 Db 669 CTGCTGGCTTCCAGAGCCCTGTTACTGACATGAAGCTGGATGAGGCTGTGACCC 728  
 OY 738 ACCACCGGCGACCATCTGACACCTTGGACAGCGGCCACACCTTCTAGCACCTCTGA 797  
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 OY 798 CAGCACTGAGAGATGTCACCGCTCCAGTTGTTGTTGTTACAGCTGACCCCTGCTACCC 857  
 Db 789 CAGCACTGAGAGATGTCACCGCTCCAGTTGTTGTTGTTACAGCTGACCCCTGCTACCC 848  
 OY 858 CGAGACCCAGAGAGCGCTTGCCTCCAGTGAATGATGCTCTGGACCAAGTTCGCCAGAG 917  
 Db 849 CGAGACCCAGAGAGCGCTTGCCTCCAGTGAATGATGCTCTGGACCAAGTTCGCCAGAG 908  
 OY 918 AGCTCTGGCGCGGCTGTGGCGCCACACTCTCCAGAGATGCCAGCGCGCTCGGACG 977  
 Db 909 AGCTCTGGCGCGGCTGTGGCGCCACACTCTCCAGAGATGCCAGCGCGCTCGGACG 968  
 OY 978 CATGATGCTGACAGCGCGGCCGAGCTTACGAGCTGATGAGAGCGGCTCCAGCGGCG 1037  
 Db 969 CATGATGCTGACAGCGCGGCCGAGCTTACGAGCTGATGAGAGCGGCTCCAGCGGCG 1028  
 OY 1038 CTGGAAGAGTTCGTGCGGACGCTGGGGCTGCGCGGAGGAGATGGAAGCCTGGAGGT 1097  
 Db 1029 CTGGAAGAGTTCGTGCGGACGCTGGGGCTGCGCGGAGGAGATGGAAGCCTGGAGGT 1088  
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 Db 1089 GGAGATGCGCGGCTTCCGAGACAGCAGTACAGAGATGCTCAAGCGCTGGGCGGAGCA 1148  
 OY 1158 GCCCGGCGGCTTCCGAGAGCGGTTTACGCGGCGCTTGAAGCGCATGGGCTGGAGGCTGCGT 1217  
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 Db 1209 GGAAGACTTGGCGAGCGGCTGAGGCGGCGCGTGA 1245

RESULT 8  
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 LOCUS AF026070 1669 bp mRNA PRI 28-JAN-1998  
 DEFINITION Homo sapiens death receptor 3 beta (DR3) mRNA, complete cds.  
 ACCESSION AF026070  
 VERSION AF026070.1 GI:2570830  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 1669)  
 AUTHORS Warzocha, K., Ribet, P., Charlot, C., Renard, N., Colflier, B. and  
 Salles, G.  
 TITLE A new death receptor 3 isoform: expression in human lymphoid cell  
 lines and non-Hodgkin's lymphomas  
 JOURNAL Biochem. Biophys. Res. Commun. 242 (2), 376-379 (1998)  
 MEDLINE 98113360  
 REFERENCE 2 (bases 1 to 1669)  
 AUTHORS Warzocha, K., Ribet, P., Renard, N., Charlot, C., Colflier, B. and  
 Salles, G.  
 TITLE Direct Submission

JOURNAL Submitted (19-SEP-1997) Hematology, CTRH Hospitalier Lyon-Sud,

Chemin du Grand Revoyet, Pierre Benite 69495, France

## FEATURES

Source

Location/Qualifiers

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/db\_xref="taxon:9606"

/cell\_line="Mieliki"

/note="Identified in human pre-B cell line Mieliki and in patients with non-Hodgkin's lymphoma"

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/gene="DR3"

/note="Apo-3; TRAMP; LARD"

69..1349

/gene="DR3"

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/codon\_start=1

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DB 189 AAGAAGATTGCTCTTTTGTGACAGAGCTGCCAGCGGGGCACTAAGGAGGCGCT 248
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DB 249 TGCAGGAGCGCGCGGCGCACTGCTGCTGTGTGCCCAAGACACTTCTTGGCC 308
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DB 309 TGGGAGAACACCATTAATCTGATGTGCCCGCTGCCAGGCTGTGATGAGAGGCGCTC 368
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DB 489 TGCCTAGATGCGGGGCGCTGCACCGCCACACAGGCTACTGTGTCCCGCAGAGACT 548
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DB 789 CCCCTGGTACTGAGATGAAGCTGGATGGAGGCTGTGACCCACACCGGCCACCAT 848
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RESULT 9  
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LOCUS HSU94503 1355 bp mRNA PRI 15-MAY-1997  
DEFINITION Human lymphocyte associated receptor of death 2 mRNA, alternatively  
spliced, complete cds.  
ACCESSION U94503  
VERSION U94503.1 GI:2071952  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 1355)  
AUTHORS Michael, A.J., and Bell, J.I.  
TITLES LARD: a new lymphoid-specific death domain containing receptor  
regulated by alternative pre-mRNA splicing  
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)  
JOURNAL MEDLINE  
97272273  
REFERENCE 2 (bases 1 to 1355)





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DEFINITION Human lymphocyte associated receptor of death 3 mRNA, alternatively spliced, complete cds.  
ACCESSION U94504  
VERSION U94504.1 GI:2071954  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 1198)  
Screation, G.R., Xu, X.N., Olsen, A.L., Cowper, A.E., Tan, R.,  
McMichael, A.J. and Bell, J.I.  
LARD: a new lymphoid-specific death domain containing receptor  
regulated by alternative pre-mRNA splicing  
Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)  
JOURNAL 2 (bases 1 to 1198)  
MEDLINE Screation, G.R.  
REFERENCE Direct Submission  
AUTHORS Submitted (19-MAR-1997) Molecular Immunology Group, Institute of  
TITLE Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3  
JOURNAL 9DU, UK

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DEFINITION	Human lymphocyte associated receptor of death 8 mRNA, alternatively spliced, complete cds.		
ACCESSION	U94509		
VERSION	U94509.1		
KEYWORDS	GI:2071964		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1119) Screation,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I		
TITLE	LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4615-4619 (1997)		
MEDLINE	97272273		
REFERENCE	2 (bases 1 to 1119) Screation,G.R.		
AUTHORS	Direct Submission		
TITLE	Submitted (19-MAR-1997) Molecular Immunology Group, Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DU, UK		
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QY	61	GGGGCCGGGGCCCAAGGCGGACACTGTAGCCCAAGTGTACTGTGCGCGTACTTCCAC	120

Db	61	GGGGCCCGGGCCCAAGGGGCGGACTCGTAGCCCAAGGTGTGACTGTGCCTGGTACTTTCCAC	120
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Db	121	AAGAAATTTGGCTGTGTTTGTGTGCAGAGGCTGCCACCGGGGCACTACTGAAGGCCCT	158
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Db	166	CAGGTGGCGCTGAGAACTGTTCAGCAAGTGGCGACACCGCGCTGTGGCTGTAAAGCCAGC	225
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 DEFINITION Human lymphocyte associated receptor of death 4 mRNA, alternatively  
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 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
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 REFERENCE  
 1 (bases 1 to 1087)  
 Screaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R.,  
 McMichael,A.J. and Bell,J.I.  
 LARD: a new lymphoid-specific death domain containing receptor  
 regulated by alternative pre-mRNA splicing  
 Proc. Natl. Acad. Sci. U.S.A. 94 (9), 4613-4619 (1997)  
 2 (bases 1 to 1087)  
 Screaton,G.R.  
 Direct Submission  
 Submitted (19-MAR-1997) Molecular Immunology Group, Institute of  
 Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3  
 9DU, UK  
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 QY 601 TTCTGGGTTCAGAGTGTCTCTGCTGCTGCTGTGTGTGTCCTCTGCTGTTGGGCCACCTTG 660  
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 Db 543 -----  
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DB 1201 GGGCTGGAAGGCTGCGTGAAGACTTGGCGCAGCGCGCTGACGCGCGCCGCTGA 1254
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RESULT 2
X00925 standard; cDNA; 1254 BP.
ID X00925:
AC X00925:
DE 25-MAR-1999 (first entry)
DE Death domain containing receptor polypeptide (DR3) encoding cDNA.
OS Homo sapiens.
FH Key CDS
FT CDS
FT sig_peptide
FT /product= "Death domain containing receptor DR3"
FT /tag= a
FT mat_peptide
FT /tag= b
FT /tag= c
PN J1100170-A.
PD 06-JAN-1999.
PE 12-MAR-1997; 057503.
PR 06-FEB-1997; US-037341.
PR 12-MAR-1996; US-013285.
PR 17-OCT-1996; US-028711.
PA (HUMA-) (HUMAN GENOME SCI INC.
PA (UNMI-) (UNIT MICHIGAN.
DR WP1: 99-124390/11.
DR P-PSDB; W95538.
PT New death domain containing receptor and recombinant vector -
PT optionally comprising leader sequence
PS Claim 6; Fig 3; 50pp; Japanese.
CC The invention provides nucleotide sequences encoding death domain
CC containing receptor polypeptides DR3-VI and DR3. The DR3-VI cDNA clone
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising
CC the nucleic acid sequences and optionally the leader sequences are
CC used for the recombinant production of the proteins. The present
CC sequence represents a cDNA encoding the death domain containing
CC receptor polypeptide (DR3).
SQ Sequence 1254 BP; 201 A; 420 C; 407 G; 226 T;

Query Match 100.0%; Score 1254; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 4,3e-263;
Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 ATGAGACAGCGCGCGGGGCTGCGCGGCGGTGGCGGGCGGCTCTCTGCTGCTG 60
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OY 301 CAGGTGGCGTGGAGACTGTTCAGAGTGGCCAGACCCGCTGGGCTGTAAAGCAGGC 360
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DB 301 CAGGTGGCGTGGAGACTGTTCAGAGTGGCCAGACCCGCTGGGCTGTAAAGCAGGC 360
OY 361 TGGTTTGGAGTGCAGAGTGCAGCAATGTGTGAGAGTTCACCTTCTACTGCCAACCA 420

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Db	361	TGGTTTGGAGTGC	CCAGGTCAGCAAT	TGTCAGCAGTT	CACCTTCTACTG	CCAAACA	420
QY	421	TGCCTAGACTG	CGGGGCCCCCTG	CACCGCCACACAGGCT	ACTGTGTTCCG	CAGAGTA	480
Db	421	TGCCTAGACTG	CGGGGCCCCCTG	CACCGCCACACAGGCT	ACTGTGTTCCG	CAGAGTA	480
QY	481	GACTGTGGGAC	CTGCTCGGCTTCT	TATGAACAT	TGGGATGGG	CGTGTGCTTCC	540
Db	481	GACTGTGGGAC	CTGCTCGGCTTCT	TATGAACAT	TGGGATGGG	CGTGTGCTTCC	540
QY	541	ACGAGCACCCT	TGGGGAGCTGTG	CAGAGCGCTGTG	CCGCTTCTGTGGCT	TGGAGGACATG	600
Db	541	ACGAGCACCCT	TGGGGAGCTGTG	CAGAGCGCTGTG	CCGCTTCTGTGGCT	TGGAGGACATG	600
QY	601	TTCTGGGTC	CAGGTGCTTC	TGCGCTTG	GGCTTGTGCTT	GGGCGCACCTG	660
Db	601	TTCTGGGTC	CAGGTGCTTC	TGCGCTTG	GGCTTGTGCTT	GGGCGCACCTG	660
QY	661	ACCTAACAT	ATCCGCGCACTG	TGGCCCTGC	AACGCCCTGGT	ATCTGCAGATG	720
Db	661	ACCTAACAT	ATCCGCGCACTG	TGGCCCTGC	AACGCCCTGGT	ATCTGCAGATG	720
QY	721	ATGAGAGCT	GTGACCCCAACACCGG	CCACCATCTG	CACCTTGTGA	CACAGCGCCACAC	780
Db	721	ATGAGAGCT	GTGACCCCAACACCGG	CCACCATCTG	CACCTTGTGA	CACAGCGCCACAC	780
QY	781	CTTCTAGAC	CTCTCTGACAGC	AGTGAGAA	GTCTGCACCGT	CTCAGTTGGTGGT	840
Db	781	CTTCTAGAC	CTCTCTGACAGC	AGTGAGAA	GTCTGCACCGT	CTCAGTTGGTGGT	840
QY	841	TGGAACCCCT	GCTACCCCCAGAC	CCAGAGGCGCT	CTGCCGCA	AGGTGACATG	900
Db	841	TGGAACCCCT	GCTACCCCCAGAC	CCAGAGGCGCT	CTGCCGCA	AGGTGACATG	900
QY	901	GACCAATGG	CCACACAGAGCT	TTGGGCCGCGT	GCACACCTG	CGCCAGAGTCC	960
Db	901	GACCAATGG	CCACACAGAGCT	TTGGGCCGCGT	GCACACCTG	CGCCAGAGTCC	960
QY	961	CCAGCAGCT	CGCCAGCCATG	ATGATCTG	CAGCCGCGC	CGCAGCTTAC	1020
Db	961	CCAGCAGCT	CGCCAGCCATG	ATGATCTG	CAGCCGCGC	CGCAGCTTAC	1020
QY	1021	CGCGTCC	CAGCGCGCGCT	GTGAAGAGT	TGTGTGCG	CACGCTGGGCGT	1080
Db	1021	CGCGTCC	CAGCGCGCGCT	GTGAAGAGT	TGTGTGCG	CACGCTGGGCGT	1080
QY	1081	ATCGAAC	CCGCGGAGGTG	AGATCGCGCTT	CCGAGAC	AGATACGAGATG	1140
Db	1081	ATCGAAC	CCGCGGAGGTG	AGATCGCGCTT	CCGAGAC	AGATACGAGATG	1140
QY	1141	CGCTGG	CGCCAGCAGCGCC	CGCGGCGCTT	GTGAGACCGT	TTCAGCGCGCCT	1200
Db	1141	CGCTGG	CGCCAGCAGCGCC	CGCGGCGCTT	GTGAGACCGT	TTCAGCGCGCCT	1200
QY	1201	GGGCTG	GACGAGCGCTG	CGTGAAGACTT	GCGAGCGCCT	TGACGCGCGCCG	1254
Db	1201	GGGCTG	GACGAGCGCTG	CGTGAAGACTT	GCGAGCGCCT	TGACGCGCGCCG	1254
RESULT	3						
TS91180							
ID	TS91180	standard; cDNA; 1634 BP.					
AC	TS91180:						
DT	14-Apr-1998	(first entry)					
DE	Human apoptosis protein Apo-3	cDNA clone FH20.57.					
KM	Apo-3; apoptosis; human; therapy; drug screening; ss.						
OS	Homo sapiens.						
FH	key	Location/Qualifiers					
FT	CDS	89..1342					
FT		/*tag= a					
FT		89..160					
FT	sig-peptide	/*tag= b					

FT		/note= "determined by hydropathy analysis"
FT	mat_peptide	161..139
FT		//tag= c
PV	W09737020-A1.	
PD	09-OCT-1997.	
PE	31-MAR-1997:	U05230.
PR	23-SEP-1996:	US-710802.
PR	01-APR-1996:	US-625228.
PA	(GETH) GENENTECH INC	
P1	Ashkenazi J.	
DR	WP1: 97-503105/46.	
PT	Polypeptide(s)	Apo-3 and Apo-2LI - useful for regulating apoptosis
PS	p11	
PT	in mammalian cells	
RS	Example 1; Page 45-46;	70pp; English.
CC	cDNA clone Fti20_57 (ATCC 55820)	codes for a novel polypeptide (see W26709), designated Apo-3,
CC	that stimulates or induces apoptotic activity	in mammalian cells.
CC	It was isolated from a human foetal heart cDNA library	by screening with probes (see G91183-84) based on an EST sequence (GenBank locus M71984) that showed homology to the intracellular domain of human TNFR1 and CD95.
CC	Amino acid residues 1-181 of Apo-3 are identical to another novel apoptosis polypeptide, Apo-2LI (see W26708).	Nucleic acids encoding Apo-3 can be used diagnostically for tissue-specific typing and to produce recombinant Apo-3 polypeptides, especially the extracellular domain (amino acids 1-198) or death domain (amino acids 338-417). Apo-3 can be used to induce apoptosis or NF-kappa-B or JNK-mediated gene expression for therapeutic purposes.
CC	Non-human transgenic animals containing cells that express Apo-3 nucleic acid, and knockout animals containing cells that have an altered Apo-3 gene, can be used in drug screening and development.	
SQ	Sequence	1634 BP; 300 A; 528 C; 519 G; 287 T;
<hr/>		
Query Match 100.0%; Score 1254; DB 1; Length 1634;		
Best Local Similarity 100.0%; Pred. NO. 4.5e-263;		
Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ATGGAGCAGCGCGGCCGCGGCCTGCGCGCGGTGGGCGCGCTTCTTGTCGTG	60
Db	89 ATGGAGCAGCGCGGCCGCGGCCTGCGCGCGGTGGGCGCGCTTCTTGTCGTG	148
QY	61 GGCGCGCGGCCCGACGCGCACTGTATGCCACAGTTGACTGTGCGGTGACTTCA	120
Db	149 GGCGCGCGGCCCGACGCGCACTGTATGCCACAGTTGACTGTGCGGTGACTTCA	208
QY	121 AAGAAGATTGCTCTGTTTGTGACAGAGCGGCCAAGCGGGCACTACTGAAGCCCCT	180
Db	209 AAGAAGATTGCTCTGTTTGTGACAGAGCGGCCAAGCGGGCACTACTGAAGCCCCT	268
QY	181 TGACAGGAGCCCTGGGCGCACTCCACCTGCTGTGTCTCCCAAGAACCTTTTGACC	240
Db	269 TGCAOGGAGCCCTGGGCGCACTCCACCTGCTGTGTCTCCCAAGAACCTTTTGACC	328
QY	241 TGGGAGAACAACCATTAATTCTGAAATGTGCCCGCTGCCAGGCGCTGTATGACAGGCGTCC	300
Db	329 TGGGAGAACAACCATTAATTCTGAAATGTGCCCGCTGCCAGGCGCTGTATGACAGGCGTCC	388
QY	301 CAGGTGGCGCTGGAGAACTGTTCACAGTATGGCCCAACCCGCTGTGGCTGTAAAGCAGGC	360
Db	389 CAGGTGGCGCTGGAGAACTGTTCACAGTATGGCCCAACCCGCTGTGGCTGTAAAGCAGGC	448
QY	361 TGGTTTGTGGAGTAGCAGGTGAGCAATGTGTACAGACAGTTACCTTTACTAGGCCAACCA	420
Db	449 TGGTTTGTGGAGTAGCAGGTGAGCAATGTGTACAGACAGTTACCTTTACTAGGCCAACCA	508
QY	421 TGCCTAGACTGCGGGGCCCTCACCGCCACACAGGCTACTCTGTTTTCCGAGAGATACT	480
Db	509 TGCCTAGACTGCGGGGCCCTCACCGCCACACAGGCTACTCTGTTTTCCGAGAGATACT	568
QY	481 GACTGTGGGAACTGCTGCTTGCTTATATGAACATGGCGCATGGCTGCTGCTCCGCC	540
Db	569 GACTGTGGGAACTGCTGCTTGCTTATATGAACATGGCGCATGGCTGCTGCTCCGCC	628

QY 541 ACAGACACCTGGGAGCTGTCCAGAGCGCTGCGGCTGTCTGTGGCTGGAGGCAGATG 600  
 DB 629 ACAGAGACACCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTCTGTGGCTGGAGGCAGATG 688  
 QY 601 TTCTGGGTCAAGTGTGCTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 660  
 DB 689 TTCTGGGTCAAGTGTGCTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 748  
 QY 661 ACCTACACATACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 749 ACCTACACATACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 808  
 QY 721 ATGAGAGCTGTGACCCACACCGGCGCCACCAATCTGTACCCCTTGGAGAGGCCACACCC 780  
 DB 809 ATGAGAGCTGTGACCCACACCGGCGCCACCAATCTGTACCCCTTGGAGAGGCCACACCC 868  
 QY 781 CTCTGTACACCTCTCTGTACAGCAGTGAAGATCTGACACCTCTCAAGTTGTGTGTTAACAGC 840  
 DB 869 CTCTGTACACCTCTCTGTACAGCAGTGAAGATCTGACACCTCTCAAGTTGTGTGTTAACAGC 928  
 QY 841 TGGACCCCTTGGCTACCCGAGACCCAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
 DB 929 TGGACCCCTTGGCTACCCGAGACCCAGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTG 988  
 QY 901 GACCACTTGGCTGACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 989 GACCACTTGGCTGACAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1048  
 QY 961 CCAGCCGCTGCGCAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
 DB 1049 CCAGCCGCTGCGCAGAGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1108  
 QY 1021 GCGGTCCACAGCGGCGCTGGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080  
 DB 1109 GCGGTCCACAGCGGCGCTGGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1168  
 QY 1081 ATGGAACCCGCTGGAAGAGT 1140  
 DB 1169 ATGGAACCCGCTGGAAGAGT 1228  
 QY 1141 CGCTGGCGCAGCAGCAGCCGCGGCTGAGAGCCGTTTACGCGGCGCTGAGCGCATG 1200  
 DB 1229 CGCTGGCGCAGCAGCAGCCGCGGCTGAGAGCCGTTTACGCGGCGCTGAGCGCATG 1288  
 QY 1201 GCGCTGACAGGCTGCTGGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1254  
 DB 1289 GCGCTGACAGGCTGCTGGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1342

RESULT 4  
 V28700  
 ID V28700 standard: cDNA; 1847 BP.  
 AC V28700;  
 DT 20-AUG-1998 (first entry)  
 DE Human apoptosis inducing receptor coding sequence.  
 KW Apoptosis inducing receptor; Air protein; human; cell death regulator;  
 KM Type I transmembrane protein; tumour cell death; autoimmune disease;  
 KW therapy; ss.  
 OS Homo sapiens.  
 FH key  
 FT Location/Qualifiers  
 FT 236..1489  
 FT /\*tag= a  
 FT CDS  
 FT /product= AIR  
 FT  
 FT W09814565-A1.  
 FT PD 09-APR-1998.  
 FT PR 03-OCT-1997; U17876.  
 FT PR 04-OCT-1996; U8-044456.  
 FT PA (IMMUNEX-CORP.  
 FT PERKINS, PA.  
 FT WPI: 98-240077/21.  
 FT DR P-PSDB; W57045.  
 FT DNA encoding apoptosis inducing receptor - which is Type I

PT transmembrane protein, useful for regulating cell death  
 PS Claim 2: Page 28-30: 45pp; English.  
 CC This sequence encodes the human apoptosis inducing receptor (AIR) of the  
 CC invention. AIR is a Type I transmembrane protein, soluble forms of which  
 CC can be used to regulate cell death in a therapeutic setting. Soluble AIR  
 CC can also be used in vitro to block apoptosis or AIR-expressing cells, or  
 CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain  
 CC of AIR can be used to develop assays for inhibitors of AIR-induced cell  
 CC death, which is useful to regulate cell death in a therapeutic setting as  
 CC well as in vitro. Agonists of AIR activity can be used to kill tumour  
 CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.  
 SQ Sequence 1847 BP; 316 A; 605 C; 579 G; 347 T.

Query Match 100.0%; Score 1254; DB 1; Length 1847;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-263;  
 Matches 1254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGCAGCGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCG 60  
 DB 236 ATGAGAGCAGCGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTGCG 295  
 QY 61 GGGGCG 120  
 DB 296 GGGGCG 355  
 QY 121 AAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGCGCGCGCGCGCGCGCGCGCGCGCT 180  
 DB 356 AAGAAGATTGGTCTGTTTGTGTCAGAGGCTGCCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCT 415  
 QY 181 TGCACGAGACCCCTGCGGCACTCCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
 DB 416 TGCACGAGACCCCTGCGGCACTCCACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 475  
 QY 241 TGGGGAACCAACCAATTTGAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 300  
 DB 476 TGGGGAACCAACCAATTTGAATGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 535  
 QY 301 CAGGTGGCGCTGAGAACATGTTTACAGCAGTGGCGCAGACCGCGCTGTGAGCTGTAAAGCAGGC 360  
 DB 536 CAGGTGGCGCTGAGAACATGTTTACAGCAGTGGCGCAGACCGCGCTGTGAGCTGTAAAGCAGGC 595  
 QY 361 TGGTTTGTGAGATGTCAGAGTACGCCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420  
 DB 596 TGGTTTGTGAGATGTCAGAGTACGCCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 655  
 QY 421 TGCCTAGACTGGGGGCGCTGTGACCGCGCAGACAGGGCTACTGTGTGTGTGTGTGTGTGTGTGTGT 480  
 DB 656 TGCCTAGACTGGGGGCGCTGTGACCGCGCAGACAGGGCTACTGTGTGTGTGTGTGTGTGTGTGTGT 715  
 QY 481 GACTGTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 DB 716 GACTGTGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 775  
 QY 541 ACAGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
 DB 776 ACAGACACCCCTGGGAGCTGTCCAGAGCGCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 835  
 QY 601 TTCTGGGTCAAGTGTGCTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 660  
 DB 836 TTCTGGGTCAAGTGTGCTGCTGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 895  
 QY 661 ACCTACACATACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
 DB 896 ACCTACACATACCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 955  
 QY 721 ATGAGAGCTGTGACCCACACCGCGCACCAATCTGTACACCTTGGAGACGCCGCCACACCC 780  
 DB 956 ATGAGAGCTGTGACCCACACCGCGCACCAATCTGTACACCTTGGAGACGCCGCCACACCC 1015  
 QY 781 CTCTGTACACCTCTGTACAGCAGTGAAGATCTGACACCGCTGAGTTGGTGGTTAACAGC 840  
 DB 1016 CTCTGTACACCTCTGTACAGCAGTGAAGATCTGACACCGCTGAGTTGGTGGTTAACAGC 1075





Db 1215 CTGACGCGGCGGCGAGCTCTAAGACGTATGAGACGCGGTCCAGCGCGCGCTGGAAAG 1274  
QY 1045 GAGTTGCTGCGACGCTGGGGGCTGCCGAGCAGATCCAGAGCCGCTGGAGTGGAGATC 1104  
Db 1275 GAGTTGCTGCGACGCTGGGGGCTGCCGAGCAGATCCAGAGCCGCTGGAGTGGAGATC 1334  
QY 1105 GGCCTGCTCCGAGACGACAGTACGATGCTCAAGCGCTGGGCGCCAGCAGACCCGCG 1164  
Db 1335 GGCCTGCTCCGAGACGACAGTACGATGCTCAAGCGCTGGGCGCCAGCAGACCCGCG 1394  
QY 1165 GGCCTGCTCCGAGACGCTTTAAGCGCGCTGGAGCGCATGGGGCTGAGAGCGCTGCGTGAAGAC 1224  
Db 1395 GGCCTGCTCCGAGACGCTTTAAGCGCGCTGGAGCGCATGGGGCTGAGAGCGCTGCGTGAAGAC 1454  
QY 1225 TTGGCGACGCGCGCTGACGCGCGCGCGTGA 1254  
Db 1455 TTGGCGACGCGCGCTGACGCGCGCGCGTGA 1484

## RESULT 6

Id X00924 standard; cDNA; 1783 BP.  
AC X00924;  
DT 25-MAR-1999 (first entry)  
DE Death domain containing receptor polypeptide (DR3-V1) encoding cDNA.  
KW Death domain: receptor; DR3-V1; DR3; recombinant; ds.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 198..1484  
FT FT /\*tag- a  
FT sig\_peptide /\*product= "Death domain containing receptor DR3-V1"  
FT FT 198..300 /\*tag- b  
FT mat\_peptide 301..1481 /\*tag- c  
FT FT J11000170-A.  
PN 06-JAN-1999.  
PD 06-FEB-1997; 057503.  
PE 12-MAR-1997; US-037341.  
PR 06-FEB-1997; US-013285.  
PR 12-MAR-1996; US-028711.  
PR 17-OCT-1996; US-028711.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PA (ONMI) UNIV MICHIGAN.  
DR WPI; 99-124390/11.  
DR P-PSDB; W95537.  
PT New death domain containing receptor and recombinant vector -  
PT optionally comprising leader sequence  
PS Claim 2; Fig 1, 2; 50bp; Japanese.  
CC The invention provides nucleotide sequences encoding death domain  
CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone  
CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is  
CC contained in ATCC deposition No. 97757. Recombinant vectors comprising  
CC the nucleic acid sequences and optionally the leader sequences are  
CC used for the recombinant production of the proteins. The present  
CC sequence represents a cDNA encoding the death domain containing  
CC receptor polypeptide (DR3-V1).  
SQ Sequence 1783 BP; 330 A; 562 C; 564 G; 327 T;

Query Match 97.1%; Score 1217.2; DB 1; Length 1783;  
Best Local Similarity 99.3%; Pred. No. 4.2e-253;  
Matches 1222; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 25 GCGGGGCTGGGGGCGGCTCTCTCTGCTGCTGGGGGCGCGGCGCGGCGGCGACT 84  
Db 255 GACCTGTGCCCCCAGGCGCTCTCTCTGCTGCTGGGGGCGCGGCGCGGCGGCGACT 314  
QY 85 CGTAGCCCCAGGTGTGACTGTGCGCGGTGACTTCCACAAGAGATTGCTGTTTGTTCG 144  
Db 315 CGTAGCCCCAGGTGTGACTGTGCGCGGTGACTTCCACAAGAGATTGCTGTTTGTTCG 374  
QY 145 AGAGCTGCCAGCGGGGCGACTACTGAAAGGCCCTTGCAGAGGAGCCCTGCGGCGCAATCC 204

Db 375 AGAGCTGCCAGCGGGGCGACTACTGAAAGGCCCTTGCAGAGGAGCCCTGCGGCGCAATCC 434  
QY 205 ACCTGCTTGTGTGTCCCAAGACACTTCTTGGCTTGGGAAACCAACATATTTCTGAA 264  
Db 435 ACCTGCTTGTGTGTCCCAAGACACTTCTTGGCTTGGGAAACCAACATATTTCTGAA 494  
QY 265 TGTGCCCGCTCCAGAGCGCTGTGATGAGCAGGCTTCCAGGTGGCGCTGGAGACTGTTCA 324  
Db 495 TGTGCCCGCTCCAGAGCGCTGTGATGAGCAGGCTTCCAGGTGGCGCTGGAGACTGTTCA 554  
QY 325 GCATGTGGCGACACCCGCTGTGGCTGTGAAGCAGGCTGGTTGGAGTGGCAGGTGAGC 384  
Db 555 GCATGTGGCGACACCCGCTGTGGCTGTGAAGCAGGCTGGTTGGAGTGGCAGGTGAGC 614  
QY 385 CAATGTGTACAGTTCACCTTCTACTGCCAACCATCCTAGACTGGCGGGCCCTGAC 444  
Db 615 CAATGTGTACAGTTCACCTTCTACTGCCAACCATCCTAGACTGGCGGGCCCTGAC 674  
QY 445 CGCCACACAGGCTACTGTTCCTCCGAGAGATCTGACTGTGGAGCTGCTGCTGCG 504  
Db 675 CGCCACACAGGCTACTGTTCCTCCGAGAGATCTGACTGTGGAGCTGCTGCTGCG 734  
QY 505 TTCTATGAACATGGGATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 564  
Db 735 TTCTATGAACATGGGATGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 794  
QY 565 GAGCGCTGTGCGCGCTGTGTGTGCTGAGAGCGAGATGTTCTGGGTCAGGTGCTCTGCT 624  
Db 795 GAGCGCTGTGCGCGCTGTGTGTGCTGAGAGCGAGATGTTCTGGGTCAGGTGCTCTGCT 854  
QY 625 GGCCTTGTGGTCCCT 684  
Db 855 GGCCTTGTGGTCCCT 914  
QY 685 COTCAAGAGCCCTGCTTACTGACATGATGAAGCTGGAGTGAAGGAGGCTTGAACCCACAC 744  
Db 915 COTCAAGAGCCCTGCTTACTGACATGATGAAGCTGGAGTGAAGGAGGCTTGAACCCACAC 974  
QY 745 GCCACCATCTGTCACTTGTGAGACGCGCCACACCTTCTGACACTTCTGACAGCACT 804  
Db 975 GCCACCATCTGTCACTTGTGAGACGCGCCACACCTTCTGACACTTCTGACAGCACT 1034  
QY 805 GAGAAGATGTGACCGCTGACAGTTGGTGGTAAACAGCTGGACCCCTGGGCTCCAGAGC 864  
Db 1035 GAGAAGATGTGACCGCTGACAGTTGGTGGTAAACAGCTGGACCCCTGGGCTCCAGAGC 1094  
QY 865 CAGGAGGCGCTTGCCTGCGGAGGTGACATGCTTGGGACAGTTGGCCAGAGCTCTT 924  
Db 1095 CAGGAGGCGCTTGCCTGCGGAGGTGACATGCTTGGGACAGTTGGCCAGAGCTCTT 1154  
QY 925 GGCCTGCTGTGCGGCCACTCTTCCAGAGTCCAGAGCGCGCTGCCAGCATGATG 984  
Db 1155 GGCCTGCTGTGCGGCCACTCTTCCAGAGTCCAGAGCGCGCTGCCAGCATGATG 1214  
QY 985 CTGCAAGCGGGGCGGAGCTTACAGAGTGAAGCGGCTCCAGCGGGGCGGTGAAG 1044  
Db 1215 CTGCAAGCGGGGCGGAGCTTACAGAGTGAAGCGGCTCCAGCGGGGCGGTGAAG 1274  
QY 1045 GAGTTGCTGCGACGCTGGGGCTGCGCGAGGCGAGAGATGAAAGCCCTGGAGTGGAGATC 1104  
Db 1275 GAGTTGCTGCGACGCTGGGGCTGCGCGAGGCGAGAGATGAAAGCCCTGGAGTGGAGATC 1334  
QY 1105 GGCCTGCTCCGAGACGACAGTACGATGCTCAAGCGCTGGGCGCCAGCAGACCCGCG 1164  
Db 1335 GGCCTGCTCCGAGACGACAGTACGATGCTCAAGCGCTGGGCGCCAGCAGACCCGCG 1394  
QY 1165 GGCCTGCGAGCGTTTACCGCGCGCTGAGAGCGATGGGCTGGAGCGCTGCGTGAAGAC 1224  
Db 1395 GGCCTGCGAGCGTTTACCGCGCGCTGAGAGCGATGGGCTGGAGCGCTGCGTGAAGAC 1454  
QY 1225 TTGGCGACGCGCTGACGCGCGCGTGA 1254  
Db 1455 TTGGCGACGCGCTGACGCGCGCGTGA 1484





Db	1248	CACGCTGGAG6CTGCTGGAGACGCCTGCTCGCGCAGCATGCACTGTCTGGCT	1297
RESULT	10		
ID	Q20973		
AC	Q20973 standard; DNA; 2062 BP.		
DT	11-MAY-1992 (first entry)		
DE	TNF-alpha binding protein gene.		
KW	Tumour necrosis factor alpha; autoimmune diseases; cachectin; ss;		
OS	extracellular domain.		
Homo sapiens.			
FH	Key	Location/Qualifiers	
FT	cds	155..1522	
FT		/tag= a	
FT	signal_peptide	155..274	
FT		/tag= b	
FT	mat_peptide	275..1522	
FT		/tag= c	
FT		473..532	
FT	misc-feature	/tag= d	
FT		/note= "homologous to probe Q20974"	
FT	misc-feature	242..751	
FT		/tag= e	
FT		/note= "encodes the extracellular domain of human TNF alpha receptor."	
FT			
PN	GB2246569-A.		
PD	05-FEB-1992.		
PF	15-JUN-1990; 013410.		
PR	15-JUN-1990; GB-013410.		
PA	(CHAR-) CHARING CROSS SUNLE.		
P1	Feldman M, Gray P, Turner M, Brennan F;		
DR	WPI; 92-043613/06.		
DR	P-PDSB; R20787.		
PT	New tumour necrosis factor alpha binding protein and polypeptide		
PT	- useful in treating cachexia, sepsis and auto immune diseases		
PT	e.g. rheumatoid arthritis		
PS	Disclosure; Fig 1; 25pp; English.		
CC	The sequence is that of DNA encoding tumour necrosis factor alpha		
CC	binding protein which was obt. from a human placental cDNA library		
CC	in lambda gtl1 using a probe (Q20974). The DNA also encodes the		
CC	extracellular domain of human TNF alpha receptor and as such it is		
CC	useful for treating diseases where TNF alpha is involved as a		
CC	causative agent, e.g. cachexia, sepsis and autoimmune diseases,		
CC	specifically Rheumatoid arthritis. See also Q20974.		
SQ	Sequence 2062 BP; 429 A; 616 C; 573 G; 444 T;		
Query Match	5.3%; Score 66.8; DB 1; Length 2062;		
Best Local Similarity	55.7%; Pred. No. 4.1e-06;		
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;			
OY	996 CCCGAGCTCTACGACGTCATGATGAGCGCGTCCACGCGCGGCCCTGGAAAGATTGCTGCG	1055	
DB	1222 CGCGAGCGCTGTAAGCGCGTGCTGTGAACAAGCTGCCCCCTTTGCCCTGGAAAGATTGCTGCG	1281	
OY	1056 CACGCTGGGGGCGCGCGAGCGAGATGCAAGCCGCGAGCGTGAGATGCGCGCTCCG	1115	
DB	1282 GCGCCTTAGGGCTGAGACGACACAGAATCATGTGCGCTGAGACTGCAGAACGGCGCTGCTT	1341	
OY	1116 AGACAGCAGTAGTACGANTGCTCAAGCGCTGCGCGCAGCAGCAGCACGCCCGCGGCTCTGAGAC	1175	
DB	1342 GCGCGAGCGCGCAATAACAGATGCTGCGCACCTGGAGCGCGCGCCGCGCGCGAGGCG	1401	
OY	1176 CGTTTACGCGCGCCCTGGAGCGCATGCGGGCTGAGACGGCTGCTGGAAGACT	1225	
DB	1402 CACGCTGAGCTGCTGGAGACGCGTCTCGCGACATGACACTGTGCGCT	1451	
RESULT	11		
ID	Q24440		
AC	Q24440 standard; DNA; 2062 BP.		
ID	Q24440;		

Query Match	5.3%	Score 66.8	DB 1	Length 2062
Best Local Similarity	55.7%	Pred. No. 4.1e-06		
Matches 128	Conservative 0	Mismatches 102	Indels 0	Gaps 0
996	CCCGCAGCTCTACGACGTGATGAGCGGTCGCCAGCGCGGCGCTGGAGAAGATTCTGCGC	1055	05-NOV-1992 (first entry)	
DB	1222	CGCGACGGCTGTACGCGTGTGTGAGAACGTCGCCCGCTTGCGCTGGAGAAGATTCTGCGC	1281	Encodes TNF-alpha 55KD receptor.
QY	1056	CACGCTGGGCGTCGCCGAGAGATCGAACCCGTCGAGAGGTGAGATCGCCCGCTTCCG	1115	tumour necrosis factor alpha: extracellular binding domain;
DB	1282	GGCGCTAGGCGTGACGACACACAGATGATCGGTGGGAGCTGCGAGAAAGGCGCGCTCT	1341	treatment: pulmonary diseases; septic shock; HIV infection; AIDS;
QY	1116	AGACGAGCATGTCGAGATGCTCAAGCGCTGGGCGCAGCGAGCCCGCGGCGCTCGGAGC	1175	malaria: viral meningitis; graft versus host disease;
DB	1342	GGCGAGGCGCATATACGATCTGTGCGACCTGTGAGAGCGGCGCCACGCCCGGCGCGAGGC	1401	autoimmune disease; Rheumatoid arthritis.
QY	1176	CGTTACGGCGGCGCTGAGCGCATGGGCGTGGACGCGTCTCTGGAAGATT	1225	Homo sapiens.

DB 1402 CACGCTGAGCTGCTGGACGCGTGTCCGACATGAGCTGTGGGCT 1451

RESULT 12

ID 010883 standard; cDNA; 2088 BP.

AC 010883;

DT 13-MAY-1991 (first entry)

DE 30KD TNF inhibitor precursor gene in lambda-gt10-7ctnfp.

KM Tumour necrosis factor; inhibitor; ss.

OS Homo sapiens.

EH Key

FT Location/Qualifiers

FT 171..1536

FT /\*tag= a

PN A09058976-A.

PD 24-JAN-1991.

PF 16-JUL-1990; 058976.

PR 18-JUL-1989; US-381080.

PR 11-DEC-1989; US-450329.

PR 07-FEB-1990; US-479661.

PA (SYNE-) SYNERGEN INC.

DR WPI; 91-073847/11.

DR P-PSDB; R10986.

PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha

PT and -beta, useful as therapeutic agent.

CC Disclosure; Fig 21, 142pp; English.

CC The sequence encodes the entire 30 KD TNF inhibitor. The clone from

CC which the sequence was obt'd. was isolated from a cDNA library

CC prep'd. from RNA form 0937 cells treated with PMA/PMA. The whole

CC gene can be inserted into expression vectors for prep'n. of TNF

CC inhibitor for use in the treatment of inflammatory and degenerative

CC diseases.

CC See also 010878, 010884 and 010907.

SO Sequence 2088 BP; 439 A; 626 C; 578 G; 445 T;

Query Match 5.3%; Score 66.8; DB 1; Length 2088;

Best Local Similarity 55.7%; Pred. No. 4.1e-06;

Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

OY 996 CCCGACGCTCTACGACGTGATGAGACGGGCTCCACGCGGGCTGGAGAGATTGCTGCG 1055

DB 1236 CGCGACGCTGTACCGCGGTGGAGAAAGTCCCGCTGGGAGAAATTGCTGCG 1295

OY 1056 CAGCGTGGGGCTGGCGAGGAGAGATGAGAGCCGCTGGAGGATCGGCGCTTCGCG 1115

DB 1296 GCGGCTTAGGGCTGAGCGACACGAGATGATCGCTGAGCTGCGAGAAAGGCGCTGCT 1355

OY 1116 AGACGACGATGAGATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGAGAC 1175

DB 1356 GCGGAGGCGCATACAGCATGTGCGGACCTGGAGCGCGGCGCAGCGCGCGAGGCG 1415

OY 1176 CGTTACGCGGCGCTGGAGCGCATGGGCTGGAGCGCTGCGTGGAGAACT 1225

DB 1416 CACGCTGAGAGCTGCTGGAGCGCTGCTCCGACATGAGACCTGTGGGCT 1465

RESULT 13

ID 010955 standard; cDNA; 2111 BP.

AC 010955;

DT 24-MAY-1991 (first entry)

DE Encodes human 55KD TNF-binding protein.

KM Tumour Necrosis Factor; binding proteins; septic shock;

KW autoimmune glomerulonephritis; lymphokine; cytokine.

EH Key

FT Location/Qualifiers

FT 187..273

FT signal\_peptide

FT /\*tag= a

FT 274..1551

FT /\*tag= b

FT /product= 55KD TNF-BP

PD EP-417563-A.

PN 20-MAR-1991.

PF 31-AUG-1990; 116707.

PR 12-SEP-1989; CH-000319.

PR 08-MAR-1990; CH-000746.

PR 20-APR-1990; CH-001347.

PA (HOFF) HOFFMANN-LA ROCHE AG.

PI Brockhaus M, Dembic Z, Gentz R, Lesslauer W, Lotscher H;

PI Schlaeger EJ;

DR WPI; 91-081851/12.

DR P-PSDB; R11082.

PT Insoluble tumour necrosis factor binding proteins - and DNA

PT encoding them, useful in pharmaceutical prods. and for antibody

PT prodn.

PS Claim 4; Fig 1; 26pp; German.

CC Partial amino acid sequences were determined for the 55 and 75KD

CC TNF-BPs (see R11072-R11081) and oligonucleotide primers were

CC synthesised based on these partial sequences. The primers were used

CC to produce a cDNA fragment for use as a probe to screen a human

CC placental cDNA bank constructed in lambda g111. Positive clones were

CC identified and sequenced. DNA constructs comprising the TNF-BP coding

CC sequence may also contain a fragment encoding a human Ig domain.

CC Recombinant constructs are used to transform cells to confer

CC improved TNF-binding properties.

CC See also 010956.

SO Sequence 2111 BP; 445 A; 628 C; 588 G; 450 T;

Query Match 5.3%; Score 66.8; DB 1; Length 2111;

Best Local Similarity 55.7%; Pred. No. 4.1e-06;

Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

OY 996 CCCGACGCTCTACGACGTGATGAGACCGGCTCCACGCGGGCTGGAGAGATTGCTGCG 1055

DB 1254 CGCGACGCTGTACCGCGGTGGAGAAAGTCCCGCTGGGAGAAATTGCTGCG 1313

OY 1056 CAGCGTGGGGCTGGCGAGGAGATGAGAGCCGCTGGAGGATCGGCGCTTCGCG 1115

DB 1314 GCGGCTTAGGGCTGAGCGACACGATGATCGGCTGGAGCTGCGAGAAAGGCGCTGCT 1373

OY 1116 AGACGACGATGAGATGCTCAAGCGCTGGCGCCAGCAGACGCCGCGGCTCGAGAC 1175

DB 1374 GCGGAGGCGCATACAGCATGTGCGGACCTGGAGCGCGGCGCAGCGCGCGAGGCG 1433

OY 1176 CGTTACGCGGCGCTGGAGCGCATGGGCTGGAGCGCTGCGTGGAGAACT 1225

DB 1434 CACGCTGAGAGCTGCTGGAGCGCTGCTCCGACATGAGACCTGTGGGCT 1483

RESULT 14

ID 006285 standard; DNA; 2141 BP.

AC 006285;

DT 29-JAN-1991 (first entry)

DE Human Tumour Necrosis Factor-Receptor cDNA insert.

KM Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

KW lambdaTNF-R2; ratTNF-R8; ss.

OS Homo sapiens.

EH Key

FT Location/Qualifiers

FT 213..1577

FT /\*tag= a

FT /label=huTNF-R

PN EP-393438-A.

PD 24-OCT-1990.

PF 06-APR-1990; 106624.

PR 21-APR-1989; DE-913101.

PR 21-JUN-1989; DE-920282.

PA (BOEH) BOEHRINGER INGELHEIMINT.

PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratawa C;

DR WPI; 90-321987/43.

DR P-PSDB; R07451.

PT DNA encoding TNF binding protein and TNF-receptor - used in

PT tumour treatment and to understand mechanism to TNF action

PS Disclosure; Fig 91(1-2); 51pp; German.

CC ratTNF-R8 (006284) was used to screen the HS913T cDNA library.



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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 05:24:33 ; Search time 50.22 Seconds

(without alignments)  
3434.787 Million cell updates/sec

Title: US-09-314-889-3

Perfect score: 1254

Sequence: 1 ATGGACGACGGCGCGCGGGG.....GCTGACGACGGCGCGCGCTGA 1254

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/2/lna/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/lna/5C\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/lna/5D\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/lna/5E\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/lna/5F\_COMB.seq:\*  
7: /cgn2\_6/ptodata/2/lna/5G\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66.8	5.3	2062	1	US-08-050-319B-24
2	66.8	5.3	2062	3	US-08-465-982-24
3	66.8	5.3	2161	5	US-09-106-038A-1
4	66.8	5.3	2175	1	US-08-321-668-1
5	66.8	5.3	2175	2	US-08-837-941-1
6	66.8	5.3	2175	4	US-08-126-016-1
7	58.8	4.7	1956	2	US-08-762-308-10
8	48.8	3.9	20235	2	US-07-642-734C-3
9	47.2	3.8	1642	1	US-08-232-015-2
10	44.8	3.6	8051	4	US-08-576-626A-2
11	44.6	3.6	2889	2	US-08-537-002A-4
12	44.6	3.6	3600	2	US-08-537-002A-5
13	43.4	3.5	330	1	US-07-849-389-6
14	43.4	3.4	1931	4	US-09-130-114-2
15	43.4	3.4	4257	3	US-08-690-473-1
16	43.4	3.4	12001	2	US-08-458-568A-11
17	42.4	3.4	396	1	US-07-924-063A-4
18	42.4	3.4	660	4	US-08-726-306A-28
19	42.4	3.4	1157	1	US-07-709-949-1
20	42.4	3.4	4524	3	US-08-845-998-7
21	42.4	3.3	43280	3	US-08-804-227C-1
22	41.3	3.3	1312	1	US-08-205-506A-1
23	41.3	3.3	1312	6	PCT-US94-02389-1
24	41.3	3.3	2793	2	US-08-209-747-1
25	41.3	3.3	2793	2	US-08-458-298-1
26	40.3	3.2	204	1	US-07-696-051B-2

c	27	40	3.2	204	1	US-07-924-063A-2	Sequence 2, Appl
	28	40	3.2	4287	1	US-08-244-189-1	Sequence 1, Appl
	29	40	3.2	4287	2	US-08-306-651B-53	Sequence 53, Appl
	30	39.8	3.2	2338	2	US-08-425-069-1	Sequence 1, Appl
	31	39.8	3.2	2338	4	US-08-317-844B-1	Sequence 1, Appl
	32	39.6	3.2	1780	4	US-08-933-821-5	Sequence 5, Appl
	33	39.6	3.2	1780	5	US-08-960-507-5	Sequence 5, Appl
	34	39.2	3.1	28804	3	US-08-597-874-1	Sequence 1, Appl
	35	39.2	3.1	28804	5	US-09-096-942-2	Sequence 2, Appl
	36	39	3.1	1288	2	US-08-440-856A-9	Sequence 9, Appl
	37	39	3.1	20235	2	US-07-642-734C-3	Sequence 116, App
	c	38	3.1	927	4	US-08-997-080-116	Sequence 3, Appl
	c	39	3.1	927	4	US-08-997-362-116	Sequence 116, App
	c	40	3.1	985	4	US-08-997-080-161	Sequence 161, App
	c	41	3.1	985	4	US-08-997-362-161	Sequence 161, App
	c	42	3.1	1569	4	US-08-997-080-113	Sequence 113, App
	c	43	3.1	1569	4	US-08-997-362-113	Sequence 113, App
	c	44	3.1	1626	4	US-08-997-080-159	Sequence 159, App
	c	45	3.1	1626	4	US-08-997-362-159	Sequence 159, App

#### ALIGNMENTS

RESULT 1  
US-08-050-319B-24  
Sequence 24, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
M.J.C. Turner, F.M.Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050.319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2062 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 155..1519  
US-08-050-319B-24

Query Match 5.3%; Score 66.8; DB 1; Length 2062;  
Best Local Similarity 55.7%; Pred. No. 5.4e-07;  
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Oy	996	CCCGAGCCTCTACAGACTATGAGACGGATCCAGCGCGCGCGGTGGAAAGAGTTCTGGCG	1055
Db	1222	CCGGACGCTGTATGACCGCTGTGGAGAACGTCGCCCGCTTGCGCTGGGAAGGAAATTCGTGCG	1281
Oy	1056	CACGCTGGGGCTCGCGCGAGGCAACAGATCAAGCGCTGTGGAGGTGGAGATCGGCGCCTTCG	1115
Db	1282	GGCGCTAGGGCTGAGGAGGACACAGATTCGATGGGTGTGACTGGAAAGCGGCGCTGCT	1341
Oy	1116	AGACCAAGCACTACAGAGATGCTCAAGCGCTGTGGCGCCACGACAGCCGCGGGGCTCGGAGC	1175
Pb	1342	GGCGAGGGCGCAATACAGATGTGGCGACCTGGAGCGCGCGCACGCCGCGGCGCCGAGGC	1401
Oy	1176	CGTTTACGGCGGCCCTGGAGCGCATGGGGGCTGACGCGCTGGGTGGAGACT	1225
Db	1402	CACGCTGGAGCTGCTGTGGAGCGCTGTCTCCCGCAATAGACTCTGTGGGCT	1451

RESULT 2  
 US-08-465-982-24  
 : Sequence 24, Application US/08465982  
 Patent No. 5863786  
 GENERAL INFORMATION:  
 APPLICANT: M. Feldmann, P.W. Gray,  
 APPLICANT: M.J.C. Turner, F.M Brennan  
 TITLE OF INVENTION: Modified human TNFalpha (Tumor  
 NUMBER OF SEQUENCES: 57  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Reed & Robbins  
 STREET: 635 Bryant Street  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465, 982  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/050,319  
 FILING DATE: 10-May-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Robbins, Roberta L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 5150-0030  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 617-8999  
 TELEFAX: (415) 327-3231  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2062 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 155..1519  
 US-08-465-982-24

Query Match	5.3%	Score 66.8	DB 3	Length 2062
Best Local Similarity	55.7%	Pred. No. 5.4e-07		
Matches 128	Conservative 0	Mismatches 102	Indels 0	Gaps 0
996	CCCCAGGCTCAACGACGCGATGACGCGCGTCCACGCGCGCCCTGGAAAGAGTTCGTGCG	1055		

Db	1222	CCGAGACGGTATGACCCCTGGTGGAGAACGCGCCCGCTTGGCGTGGAAGAAATTTGTCGCG	1281
QY	1056	CACGCTGGGGCTGCGCGAGCCACAGATCGAAGCCCTGGAGAGTGGAGATGCGCCGCTTCCG	1115
Db	1282	GCGCCTTAGGGCTGAGCCACCCAGCAGATCGATCGCTGGAGCTGCGAAGAGGGCGCTGCTCT	1341
QY	1116	AGACCAGCAGTACGAGATGCTCAAGCGCTGGGCCACAGCACCCCGGGCGCTGGAGAC	1175
Db	1342	GCGGAGGCGGCAATACAGCATGCTGGCGACCTTGGAGGGCGGCGACCGCCGCGCGGAGGC	1401
QY	1176	CGTTTACGCGGCCCTGGAGGCGCATGGGGCTGGACGCGCTCGTGGAAAGACT	1225
Db	1402	CACGCTGGAAGCTGCTGGGAGCGCTGCTCCGCGCAGATGAGACCTGCTGGGCT	1451

RESULT 3  
 US-09-106-038A-1  
 : Sequence 1, Application US/09106038A  
 : Patent No. 6007995  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Brenda F. Baker and Lex M. Cowser  
 : TITLE OF INVENTION: ANTISENSE MODULATION OF TNFRI  
 : TITLE OF INVENTION: EXPRESSION  
 :  
 : NUMBER OF SEQUENCES: 91  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Isis Pharmaceuticals, Inc.  
 : STREET: 2292 Faraday Avenue  
 : CITY: Carlsbad  
 : STATE: CA  
 :  
 : COUNTRY: U.S.A.  
 :  
 : ZIP: 92008  
 :  
 : COMPUTER READABLE FORM:  
 :  
 : MEDIUM TYPE: 3.5 inch disk, 1.44 MB  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: Windows NT  
 :  
 : SOFTWARE: Microsoft Word 97  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/106,038A  
 : FILING DATE: June 26, 1998  
 : CLASSIFICATION: 514  
 :  
 : ATTORNEY/AGENT INFORMATION:  
 :  
 : NAME: Laurel Spear Bernstein  
 : REGISTRATION NUMBER: 37,280  
 : REFERENCE/DOCKET NUMBER: RTS-0004  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (760) 931-9200  
 : TELEFAX: (760) 603-3820  
 :  
 : INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 :  
 : LENGTH: 2161  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 :  
 : US-09-106-038A-1

[illegible]

Db 1503 CACGCTGAGCTGCTGGAGCGCTGCTCCGACATGAGACTCTGCGGCT 1552

RESULT 4  
US-08-321-668-1

; Sequence 1, Application US/08321668  
; Patent No. 5665859  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARPOLOMEYEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/321,668  
; FILING DATE: 12-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH-13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2175 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 256..1620  
; US-08-321-668-1

Query Match 5.3%; Score 66.8; DB 1; Length 2175;

Best Local Similarity 55.7%; Pred. No. 5.5e-07;  
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 996 CCCGAGCTTACGAGTGTGATGAGCGGCTCCGAGCGCGCTGGAAGATTGTCGCG 1055  
Db 1323 CCGGAGCTGTACGCTGTGTGAGAACGTGCCCTTGGCTGGAAGAAATTCGTGCG 1382  
QY 1056 CACGCTGGGCTCCGCGAGGCAAGATCGAAGCCGTGAGAGTGCAGATCGGCCCTTCG 1115  
Db 1383 GCGCCTAGGCTGAGCGACGACGATCGATCGGCTGAGACTGCAAGGAGGCGCTGCT 1442  
QY 1116 AGACGAGCATAGAGATGCTCAAGCCCTGCGCCGACACAGAGCCCGGCGCTCGAGC 1175  
Db 1443 GCGGAGGCGCAATACAGATGCTGCGGACCTGAGAGCGGCGCAAGCGCGCGAGGC 1502  
QY 1176 CGTTTACGCGGCGCTGAGCGCATGGGGCTGAGACGCTGCTGGAAGACT 1225

Db 1503 CACGCTGAGCTGCTGGAGCGCTGCTCCGACATGAGACTCTGCGGCT 1552

RESULT 5  
US-08-837-941-1

; Sequence 1, Application US/08837941  
; Patent No. 5766917  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BRAKEBUSCH, Cord  
; APPLICANT: VARPOLOMEYEV, Eugene  
; APPLICANT: BATKIN, Michael  
; TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
; TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/837,941  
; FILING DATE: 28-APR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/321,668  
; FILING DATE: 12-OCT-1994  
; APPLICATION NUMBER: IL 107268  
; FILING DATE: 12-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: WALLACH-13  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2175 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 256..1620  
; US-08-837-941-1

Query Match 5.3%; Score 66.8; DB 2; Length 2175;

Best Local Similarity 55.7%; Pred. No. 5.5e-07;  
Matches 128; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 996 CCCGAGCTTACGAGTGTGATGAGCGGCTCCGAGCGCGCTGGAAGATTGTCGCG 1055  
Db 1323 CCGGAGCTGTACGCTGTGTGAGAACGTGCCCTTGGCTGGAAGAAATTCGTGCG 1382  
QY 1056 CACGCTGGGCTCCGCGAGGCAAGATCGAAGCCGTGAGAGTGCAGATCGGCCCTTCG 1115  
Db 1383 GCGCCTAGGCTGAGCGACGACGATCGATCGGCTGAGACTGCAAGGAGGCGCTGCT 1442  
QY 1116 AGACGAGCATAGAGATGCTCAAGCCCTGCGCCGACACAGAGCCCGGCGCTCGAGC 1175  
Db 1443 GCGGAGGCGCAATACAGATGCTGCGGACCTGAGAGCGGCGCAAGCGCGCGAGGC 1502



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RESULT      8
; US-07-642-734C-3/C
; Sequence 3. Application US/07642734C
; Patent No. 5824513
; GENERAL INFORMATION:
;   APPLICANT:   Katz, L
;   APPLICANT:   Donadio, S
;   APPLICANT:   McAlpine, J B
;   TITLE OF INVENTION: Recombinant DNA Method for Producing
;   NUMBER OF SEQUENCES: 27
;   Erythromycin Analogs
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:   Edward H. Gorman
;   STREET:      Abbott Laboratories D377/AP6D-2 One Abbott
;   CITY:        Abbott Park
;   STATE:       IL
;   COUNTRY:     US
;   ZIP:         60064-3500
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/642,734C
;   FILING DATE:  17-JAN-91
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME:         Danckerts, Andreas M
;   REGISTRATION NUMBER: 32652
;   REFERENCE/DOCKET NUMBER: 4952.US.01
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:    708-937-9396
;   TELEFAX:      708-938-2623
;   INFORMATION FOR SEQ ID NO: 3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:       20235 base pairs
;   TYPE:          nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY:     unknown
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE:   NO
;   ORIGINAL SOURCE:
;   ORGANISM:      Saccharopolyspora erythraea
;   STRAIN:        NRRL 238
;   FEATURE:
;   NAME/KEY:     CDS
;   LOCATION:     19..10722
;   OTHER INFORMATION: /codon_start= 19
;   OTHER INFORMATION: /function= "gene eryA"
;   OTHER INFORMATION: /product= "eryA ORF2 encoding modules 3 & 4 for
;   OTHER INFORMATION: 6-deoxyerythronolide B"
;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     19..4470
;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: module 3"
;   FEATURE:
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;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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;   LOCATION:     1693..2670
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;   OTHER INFORMATION: acyltransferase domain module 3"
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;   FEATURE:
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;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: acyltransferase domain of module 4"
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;   LOCATION:     9433..9984
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;   OTHER INFORMATION: beta-ketoreductase of module 4"
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;   LOCATION:     10723..20235
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;   NAME/KEY:     misc_feature
;   LOCATION:     10723..15165
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;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     10831..12174
;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul"
;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     12379..13350
;   OTHER INFORMATION: /function= "approximatr span of
;   OTHER INFORMATION: acyltransferase domain of module 5"
;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     14062..14610
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;   OTHER INFORMATION: beta-ketoreductase of module 5"
;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     14857..15114
;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: acyl carrier domain of module 5"
;   FEATURE:
;   NAME/KEY:     misc_feature
;   LOCATION:     15166..20235
;   OTHER INFORMATION: /function= "approximate span of
;   OTHER INFORMATION: module 6"
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NAME/KEY: misc_feature
LOCATION: 15172..16569
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoacylACPSynthase domain of modul
FEATURE:
NAME/KEY: misc_feature
LOCATION: 16768..17721
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 18379..18921
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 6"
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NAME/KEY: misc_feature
LOCATION: 19149..19398
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FEATURE:
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LOCATION: 19492..20235
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US-07-642-734C-3

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Query Match 3.9%; Score 48.8; DB 2; Length 20235;
Best Local Similarity 46.3%; Pred. No. 0.013;
Matches 199; Conservative 0; Mismatches 227; Indels 4; Gaps 1;

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QY 825 GTGTGGTGAACAGCTGAGCCCTGACCCCGAGAGCCGAGGCGCTGCGCCGA 884
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DB 6699 GGTGATGTGCTCCAGCTGCGCCGAGCCGCTCTCGATGCGCGCCACTCGGGGAG 6640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 885 GGTGACATGTCCTGGAGACAGTTGCCAGAGAGCTCTTGGCCCGCTGCTGCGCCAC 944
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DB 6639 GGAGCCGTAAGCGACAGCGGATCCGCGGCTTCATCTCCCGCTCGGCTCGGCGAA 6580
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QY 945 ACTTCGCCAGAGTCCCAAGCCGCTCGCCAGCCATGATGCTGCAAGCCGCGCCGAGCT 1004
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DB 6579 GAACCTCGTCCAGCTCGCGGCTCGCGCCGAGCAAGAGCTGGTG---CCAGGCCGTTGA 6524
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QY 1005 CTACAGCTGATGAGCGGCGTCCAGCGGCGCTGGAAGGATTCGTCGACCTGGG 1064
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DB 6523 CGGCGGCGACCGCGACAGCGCGCTCCAGCGCGCGAGCAAGCTTCAGCTGTGCGGG 6464
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QY 1065 GCTGCGGAGGAGAGATCGAAGCCGTGGAGGTGAGATCGCGCTTCGAGACCAACA 1124
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DB 6463 ACGGCGGACCGACACATGCGCGCTGTGCTGAGCTCGCGCAACACTGCTGCGCA 6404
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QY 1125 GTACAGATGCTCAAGCGCTGCGCGAGAGAGCGCGCGCGCGCTGAGCGCTTACGC 1184
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DB 6403 GGGCCACACCTTGGCGGCTTCCAGGACAGAGCGCGCGCGCGCTGCGCGCGCA 6344
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QY 1185 GGCCTGAGAGCGATGGGCTGAGCGCTGCTGGAAGACTTGGCGAGCGCGCTGCAAGC 1244
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DB 6343 TCTGCGCTGCGAGTGGCGGAGAGAGCGCGCGCGGCTGACGCGCTGCGCGCAAGCT 6284
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DB 6283 CGGCGACGCA 6274

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RESULT 9
US-08-232-015-2/c
Sequence 2, Application US/08232015
Patent No. 5650272
GENERAL INFORMATION:
APPLICANT: GUESDON, Jean-Luc
APPLICANT: THIERRY, Dominique
APPLICANT: VINCENT, Veronique

```

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TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH HYBRIDIZE
TITLE OF INVENTION: SPECIFICALLY WITH BACTERIAL STRAINS OF THE MYCOBACTERIUM
TITLE OF INVENTION: AVIUM-INTRACELLULAR COMPLEX
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,015
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 93/09251
FILING DATE: 13-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/13504
FILING DATE: 31-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 004900-127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mycobacterium avium
US-08-232-015-2

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Query Match 3.8%; Score 47.2; DB 1; Length 1642;
Best Local Similarity 48.5%; Pred. No. 0.017;
Matches 130; Conservative 0; Mismatches 138; Indels 0; Gaps 0;
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DB 341 GCCCTGGCGGAGATATCCCGGTGACCGGATGACCGCGCATATGCTTCGCGGCATG 282
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QY 938 CGGCCACATCTTCGCCAGAGTCCCGAGCGGCTCGCCAGCCATGATGCTGCAAGCCGGGCC 997
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DB 281 GACACACACCGACCCGCGTCCGCGCGCGAGATGCGCGGATGCGCAAGTCAATG 222
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QY 998 CGAGCTTACAGCATGATGAGACGCGTCCAGCGCGCGCTGGAAGAGTTGCTGCGCA 1057
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DB 221 CGGGGCGGCTGGCGGAGAGTGTGCTTATCAGGGCGCGGCGGAGATGGGCGGG 162
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QY 1058 CGCTGGGCTGCGCGAGAGAGATGAAAGCCGTGGAGGTGAGATCGGCCCTTCCAG 1117
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DB 161 CCCAAGCGGTGGCTTCCGCAAGAGGCGCCGACATCGTGGCGCTGACCTTGGCGAG 102
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QY 1118 ACCAGCATACAGATGCTCAAGCGCTG 1145
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DB 101 CGGTGACACAGGTATGTTCCGCCAG 74

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RESULT 10

US-08-576-626A-2  
; Sequence 2, Application US/08576626A  
; Patent No. 5998194  
; GENERAL INFORMATION:  
; APPLICANT: Summers, R.G.  
; APPLICANT: Katz, L.  
; APPLICANT: Donadio, S.  
; APPLICANT: Staver, M.J.  
; TITLE OF INVENTION: POLYKETIDE-ASSOCIATED SUGAR  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/576,626A  
; FILING DATE: 21-DEC-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Diane Casulo  
; REGISTRATION NUMBER: P-40,943  
; REFERENCE/DOCKET NUMBER: 5857.US.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (847) 938-3137  
; TELEFAX: (847) 938-2623  
; TELEX:  
; INFORMATION FOR SEQ. ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8051 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-576-626A-2

Query Match 3.6%; Score 44.8; DB 4; Length 8051;  
Best Local Similarity 52.7%; Pred. No. 0.088;  
Matches 97; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 1045 GAGTTGTCGCGACGCTGGGCTGCGGAGAGATGCAACCCGTGAGGTGAGATC 1104  
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DB 2528 GAGGACGTACCGGCTGGGCTGTCGGCGCATGATGAGGTGCGCGCGGCGGACTC 2587  
QY 1105 GAGCGCTTCGAGACGACGATGACGATGCTCAAGCGCTGGGCGCGGCGGCGGCGG 1164  
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DB 2588 GCGGCGATCCCGTCTGCGAGGCGGACATGCGGACTTCGCGCTGGGATCCGAGTTGAC 2647  
QY 1165 GGCCTGAGCCCTTTACGCGCCCTGAGAGCGATGGGCTGAGCGCTGCGTGAAGAC 1224  
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DB 2648 GCGGTACCTGCATGTTCAAGCTCCATCGGCGACATGCGGCGGCGGCGGCGGCTGAGACAG 2707  
QY 1225 TTGC 1228  
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DB 2708 GCGC 2711

RESULT 11  
US-08-537-002A-4  
; Sequence 4, Application US/08537002A  
; Patent No. 5773282  
; GENERAL INFORMATION:

APPLICANT: TSUSAKI, Keiji  
APPLICANT: KUBOTA, Michio  
APPLICANT: SUGIMOTO, Toshiyuki  
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR  
TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/537,002A  
FILING DATE: 29-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 260984/1994  
FILING DATE: 01-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP No. 5773282 yet received  
FILING DATE: 08-SEP-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TSUSAKI-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2889 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-537-002A-4

Query Match 3.6%; Score 44.6; DB 2; Length 2889;  
Best Local Similarity 46.3%; Pred. No. 0.076;  
Matches 181; Conservative 0; Mismatches 209; Indels 1; Gaps 1;

QY 850 GGTACCCCGAGACCCAGAGGCGCTGTGCGGAGTGATGCTCTGGGACCAATTG 909  
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DB 2369 GCTTCCCGGCTCGGGGGGACGCGCCCGGAGCCCGAGGCTCTCCGGGGGCTGC 2428  
QY 910 CCCAGCAGAGCTCTTGGCGCCGCTGCTGCGCCACACTCTGCCAGATCCCGACGCGG 969  
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DB 2429 ACGAGACCAAGCCCTGTGCTCTCTCTGCGGGTGCCTGTGCTCTCTCTCAACGGGCCC 2488  
QY 970 TCGCAGCATGATGCTGACGCGGCGCGGCGGCGGCTTACGAGCTGATGAGCGGCTCCA 1029  
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DB 2489 TTGGGAGAGTGAAGGGGTGTGGGGGGGCGACCCCTCTCTAGCGCGCGGCTCGGCGCT 2548  
QY 1030 GCGCGCGCTGGAAGAGTGTGTGCGACGCTGGGGGCTGCGCGAGCAGAGATGAGACC 1089  
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DB 2549 TCTGTGAGCTGG-AGGGGAGAGTGTACTCTGCTGCGCTGCGGCGGGAAGGCGGCGACG 2607  
QY 1090 GTGAGGTGAGATGCGCGCTTCGAGACGAGCAGTACGAGTCAAGCGGCGGCGG 1149  
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DB 2608 GTGAGAGGAGCTGGCGCGCTGCGCTACGAGCTGAGCGGCGGCGGCTGACCTCGCTCT 2667  
QY 1150 CAGCAGAGCCCGCGGCGCTGCGAGCGCTTACGCGGCGCTGAGAGCGCATGGGCTGAGAC 1209  
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DB 2668 GAGGCGCTGAGAGGCGGAGCTTTGGGCGCTTTCGAGAGAGTGGCGGACACCTCACCGCC 2727

Qy 1210 GGCTGCGTGAAGACTTGCCGACGCCCTGC 1240  
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Db 2728 GCGTCCTCCAAGCCTACCGGTCCGCCCTTC 2758

RESULT 12

US-08-537-002A-5  
; Sequence 5, Application US/08537002A  
Patent No. 5733003

GENERAL INFORMATION:

1 APPLICANT: ISUSAKI, Keiji  
2 APPLICANT: KUBOTA, Michio  
3 APPLICANT: SUGIMOTO, Toshiyuki  
4 TITLE OF INVENTION: RECOMBINANT THERMOSTABLE ENZYME FOR  
5 TITLE OF INVENTION: CONVERTING MALTOSE INTO TREHALOSE  
6 NUMBER OF SEQUENCES: 17  
7 CORRESPONDENCE ADDRESS:  
8 ADDRESSEE: BROADY AND NEIMARK  
9 STREET: 419 Seventh Street, N.W., Suite 300  
10 CITY: Washington  
11 STATE: D.C.  
12 COUNTRY: USA  
13 ZIP: 20004

Query Match	3.6%	Score	44.6	DB 2	Length	3600
Best Local Similarity	46.3%	Pred. No.	0.08	-		
Matches 181; Conservative	0	Mismatches	209	Indels	1	Gaps 1

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Db	2909	GCTTTCCCGCCCTTCGCGGGGACAGCCCCCGGAGACCCAGGCTCTCTTCCCGGGGCCCTTGC	2968
QY	910	CCGACGAGAGCTTTTGACCCCGCTGCTGCGCCACACTCTCGCAGAGTCCCCACGCGGC	969
Db	2969	ACGAGACCGAAGGCGCTGATCTCCGCTCTCTCGGGGTGGCGCTCCCTCTCTACACGGGGCC	3028
QY	970	TCGCGACCATGATGCTGCAGCCGGGCGCCGACGCTTACAGAGTATGAGACGGTTC	1029
Db	3029	TTGGGGAGGTGAGGGGGGTGTGGTGGGGGGCACCCCCCTCTTAAGCCGCGGCTCGGGGGCT	3088
QY	1030	CGCGGGGCGTGGAAAGAGTTCGTCGCGCACGCTGGGGCTCGCGAGGACAGATCCAAACC	1089
Db	3089	TCTTGAGGCTTG-GGGGAGGTGTACTCTGTGTCCTTGCGCGGAAAAGCGGGGACAG	3147
QY	1090	GTCGAGGTGGAGATCGGCGCCCTCTCCAGACACAGCACTACGAATGCTCAAGCCGTGGGC	1149
Db	3148	GTCGAGGAGAGACCTGGCGCCGCTCGGCTTACAGAGTGGAGCGGGGCCGTGCACTCGCCTC	3207
QY	1150	CAGCAGCAGCCCCCGGGCTCTCGAGCCGTTTACGCGGCCCTGAGAGCCTATGGGCGCTGAGC	1209
Db	3208	GAGCGCTCGAGGCGGAGCTTTTGAGGCTTTTGCCGGAAGAGTGGACGACACCTTCAGCGCC	3267
QY	1210	GGTCGCGTGAAGACTTCGACAGCGGCGCTGC	1240
Db	3268	GCTCTCTCCAAAGCTTACCGCTTCGCGCTCTC	3298

RESULT 13

US-07-849-389-6  
; Sequence 6, Application US/07849389  
Patent No. 5535A03

GENERAL INFORMATION:

APPLICANT: HORNES, ELIA  
APPLICANT: UHLEN, Mathias  
TITLE OF INVENTION: CLONING METHOD AND KIT  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM: 11/11

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? INFORMATION FOR SEQ ID NO: 6
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 330 base pairs
?     TYPE: NUCLEIC ACID
?     STRANDEDNESS: single
?     TOPOLOGY: linear
?     MOLECULE TYPE: DNA (genomic)
?     ORIGINAL SOURCE:
?     ORGANISM: HUMAN LIPOPROTEIN E GENE
?     FEATURE:

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Wed Jul 26 07:05:03 2000

us-09-314-889-3.rn1

Search completed: July 23, 2000, 06:28:45  
Job time: 3852 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2000, 05:02:15 ; Search time 466.05 Seconds  
(without alignments)  
11865.518 Million cell updates/sec

Title: US-09-314-889-3

Perfect score: 1254

Sequence: 1 ATGAGCAGCGCGCGCGGG.....GCCCGCAGCGCGCGCCCGTGA 1254

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

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22: gb\_est3:\*  
23: gb\_est4:\*  
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QY	398	GTTCACCCCTTACAGCCCAACCATGCTTACAGCTGGCGGGGCGCTGCACACGGCACACACAGCG	457
Db	361	CTTACCCCTTCTACTAGCCCAACCATGCTTACAGCTGGCGGGGCGCTGCACACGGCACACACAGCG	420
QY	458	TACTTCTGTCCCGCAGAGATACTGACTGTGGGACCGCTGCTGCTTCTATGAACATG	517
Db	421	TACTTCTGTCCCGCAGAGATACTGACTGTGGGACCGCTGCTGCTTCTATGAACATG	480
QY	518	GGATGCGCTGCTGTCTTGGCCCGCAGACACCGCTGGGAGCTGTCCAGACGCTGTGCCG	577
Db	481	GGATGCGCTGCTGTCTTGGCCCGCAGACACCGCTGGGAGCTGTCCAGACGCTGTGCCG	540
QY	578	CTGTCTGTGGCTGGAGGAGCAGATGTTCTGGGCTCCAGCTGCTCTGCTGGCTTGTGTGTC	637
Db	541	CTGTCTGTGGCTGGAGGAGCAGATGTTCTGGGCTCCAGCTGCTCTGCTGGCTTGTGTGTC	600
QY	638	CCCTCTGCTGGGCGCACCGCTGACCTACACATACCGCGCAGCTGCTGCTGCTGCTGCTGCTG	697
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QY	698	TGCTTACTGACAGATGAGCTGGGATGGAGCGCTGTGC	734
Db	661	CTGCTACTGACAGATGAGCTGGGATGGAGCGCTGTGC	697
RESULT	2		
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LOCUS			
DEFINITION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			

ORIGIN	Query Match	Best Local Similarity	47.1%;	Score 591;	DB 70;	Length 632;
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QY	47	TCCTGTCCTGCTGGGGGCCCGGGGCCAGGGCCGGCAGCTCTGAGCCCCAGGTGTGACTGTG	106			
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QY	107	CCGGTGACTTCCACAAGAAGATTGGTCTGTTTGTGTGTGAGAGGCTGCCACGGGGGACT	166			
Db	61	CCGGTGACTTCCACAAGAAGATTGGTCTGTTTGTGTGTGAGAGGCTGCCACGGGGGACT	120			
QY	167	ACCTGAAGGCCCTTTGGACGAGAGCCCTGCGCACTCCACTGCGCTTGTGTGTCCTCCAG	226			
Db	121	ACCTGAAGGCCCTTTGGACGAGAGCCCTGCGCACTCCACTGCGCTTGTGTGTCCTCCAG	180			
QY	227	ACACCTTTCTTGCCCTGGGAGAACCAACCTAAATTCTGAATGTGCCCGCTGCCAGGCGCTGTG	286			
Db	181	ACACCTTTCTTGCCCTGGGAGAACCAACCTAAATTCTGAATGTGCCCGCTGCCAGGCGCTGTG	240			
QY	287	ATGAGCAGGCTCTCCAGGTGGCGCTGGAGAAGCTGTTACAGCACTGGCCGACACCCGCTGTG	346			
Db	241	ATGAGCAGGCTCTCCAGGTGGCGCTGGAGAAGCTGTTACAGCACTGGCCGACACCCGCTGTG	300			
QY	347	GCTGTAAAGCCAGGCGTGGTTTGTGAGTGCACAGTCCAGCATGTGTGTACAGATTCAACCT	406			
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QY	407	TCTACTGGCAACCATGCTAGACTGCGGGGCCCTGCACCCGACACACAGGCTACTCTGTT	466			
Db	361	TCTACTGGCAACCATGCTAGACTGCGGGGCCCTGCACCCGACACACAGGCTACTCTGTT	420			
QY	467	CCCCGACAGATACGTAGCTGTGGGACCTGCTGCTGGCTTCTATGACATGSCGATGCT	526			
Db	421	CCCCGACAGATACGTAGCTGTGGGACCTGCTGCTGGCTTCTATGACATGSCGATGCT	480			
QY	527	GCGTGTCTCTGCCCGACGACGACCCGTGGGGAGCTGTGCCAGACGGCTGTCGCTGTG	586			
Db	481	GCGTGTCTCTGCCCGACGACGACCCGTGGGGAGCTGTGCCAGACGGCTGTCGCTGTG	540			
QY	587	GCTGGAGGACAGATGTCTGGGGTCCAGAGGTCTCTGGGCTGGCTTGTGTGCCCTCTGC	646			
Db	541	GCTGGAGGACAGATGTCTGGGGTCCAGAGGTCTCTGGGCTGGCTTGTGTGCCCTCTGC	600			
QY	647	TTGGGGCCACCCCTGACCTACATACCGCCAC	678			
Db	601	TTGGAGGATCTCTGAACATACATACCTGTAC	632			
RESULT	3					
LOCUS	AI424936					
DEFINITION	AI424936	688 bp	mRNA	EST	30-MAR-1999	
ACCESSION	AI424936					
VERSION	AI424936.1					
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.					
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.					
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),					
COMMENT	Unpublished (1997)					
	Contact: Robert Strausberg, Ph.D.					
	Tel: (301) 496-1550					
	Email: Robert.Strausberg@nih.gov					



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|||||
Db 181 GCCCTGGGCAACTCCACCTGCTTGTGTGCCAAGACACCTTCTGGCTGGAGAA 240
QY 249 CCACATTAATTTCTGAATGTGCCCCCTCCAGGCTGTGATAGACAGCCTCCAGGTGC 308
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QY 309 GCTGAGAACTGTTTACACAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGGTTGT 368
Db 301 GCTGAGAACTGTTTACACAGTGGCCGACACCCGCTGTGGCTGTAAAGCCAGGCTGGTTGT 360
QY 369 GGAATGCAAGTACAGCAATGTGTACACAGTTACACCTTTACTAGCCAAACATGGCTAGA 428
Db 361 GGAATGCAAGTACAGCAATGTGTACAGAGTTACACCTTTACTAGCCAAACATGGCTAGA 420
QY 429 CTGGGGGGGGGGTACAGCCGACACAGGCTACTGTGTTCCCGACAGACTACTGACTGTGG 488
Db 421 CTGGGGGGGGGGTACAGCCGACACAGGCTACTGTGTTCCCGACAGACTACTGACTGTGG 480
QY 489 GACCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGTGCTGCTCCACAGAGCAG 548
Db 481 GACCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGTGCTGCTCCACAGAGCAG 540
QY 549 CCTGGGGAGCTGTCCAGAGCGC 570
Db 541 CCGNGAGAGCTGTCCAGAGCGC 562

RESULT 5
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DEFINITION xp93402.x1 Soares_NHCE-cervix Homo sapiens cDNA clone IMAGE:2747954
3' similar to TR:000276 000276 LYMPHOCTE ASSOCIATED RECEPTOR OF
DEATH 2.; mRNA sequence.
AM517358
VERSION AM517358.1 GI:7155440
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 489.
Location/Qualifiers
1.585
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/lab_host="Soares_NHCE-cervix"
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a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - c1190(dT) primer [5'
TGTACCAATCTGACGTGGAGCGCGCGGCTTTTGTGTGTGTGTGTGTGTGTGT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pRTT3 vector.
Library is normalized; constructed by Bento Soares and
M.Fatima Bonaldi."
BASE COUNT 94 a 181 c 193 g 117 t
ORIGIN

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Query Match 42.7%; Score 535.4; DB 73; Length 585;
Best Local Similarity 98.9%; Pred. No. 1.3e-110;
Matches 539; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 9 GCGGCGCGGGGCTGCGGGGCGGGGCGGCTCCCTCGTGTGCTCTGGGGGCGCG 68
Db 1 GCGGCGCGGGGCTGCGGGGCGGGGCGGCTCCCTCTGCTGTGCTGTGCTGGGCGCG 60
QY 69 GCGCGAGGCGGCACTGCTAGAGCCAGAGTGTACTGTGCGGCTGTCCACAGAGAAT 128
Db 61 GCGCCAGAGGCGGCACTGCTAGAGCCAGAGTGTACTGTGCGGCTGTCCACAGAGAAT 120
QY 129 TGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTAAGTGAAGGCCCTTGCACGA 188
Db 121 TGGTCTGTTTGTTCAGAGGCTGCCAGCGGGGCACTAAGTGAAGGCCCTTGCACGA 180
QY 189 GCGCTGGCGCAACTGCACCTGCTGTGTGTGCTCCCAAGACACTTGTGGCTGGAGAA 248
Db 181 GCGCTGGCGCAACTGCACCTGCTGTGTGTGCTCCCAAGACACTTGTGGCTGGAGAA 240
QY 249 CCACATTAATTTCTGAATGTGCCCCCTCCAGGCTGTGATAGACAGCCTCCAGGTGC 308
Db 241 CCACATTAATTTCTGAATGTGCCCCCTCCAGGCTGTGATAGACAGCCTCCAGGTGC 300
QY 309 GCTGAGAACTGTTTACAGAGTGGCCGACACCCGCTGTGCTGTAAAGCCAGGCTGTTGT 368
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QY 369 GGAGTGGCAGGTACAGCAATGTGTACAGAGTACACCTTCTACTGCAACCAATGGCTAGA 428
Db 361 GGAGTGGCAGGTACAGCAATGTGTACAGAGTACACCTTCTACTGCAACCAATGGCTAGA 420
QY 429 CTGGGGGGGGGGTACAGCCGACACAGGCTACTGTTTCCCGACAGACTACTGACTGTGG 488
Db 421 CTGGGGGGGGGGTACAGCCGACACAGGCTACTGTTTCCCGACAGACTACTGACTGTGG 480
QY 489 GACCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGTGCTCCACAGAGCAG 548
Db 481 GACCTGCTGCTGCTTCTATGAACATGGGATGGCTGCTGTGCTCCACAGAGT 540
QY 549 CCTGG 553
Db 541 CCTAG 545

RESULT 6
Locus AI203624 508 bp mRNA EST 29-OCT-1998
DEFINITION ge5f02.x1 Soares_fetal_lung_NHHL19W Homo sapiens cDNA clone
IMAGE:1744827 3' similar to SW:WSL1_HUMAN Q93038 WSL-1 PROTEIN
PRECUSOR; mRNA sequence.
AI203624
VERSION AI203624.1 GI:3756230
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
TITLE Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1699 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 442.

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Db	421	CCACA-ACGGCTACTGTTT-CGCGAGAGAT-CTGACTGTGGACCCTGCCTCCTTGCTT	477
RESULT	8		
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DEFINITION	A1700459	mRNA	EST
ACCESSION	A1700459		17-DEC-1999
VERSION	A1700459.1	GI:4988359	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index Unpublished (1997) On Oct 30, 1998 this sequence version replaced gi:3812616. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov This clone is available royalty-free through LNL ; contact the IMAGE Consortium (infoimage.llnl.gov) for further information. Insert Length: 1627 Std Error: 0.00 Seq primer: -40UP from Gibco High quality sequence stop: 422. Location/Qualifiers 1..422 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_xref="IMAGE:2328093" /clone_lib="Soares_NFL_T_GBC_SI" /lab_host="DH10B" /note="Organ: pooled; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-GAP GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonalato."		
BASE COUNT	66 a	132 c	139 g
ORIGIN	85 t		
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Best Local Similarity	99.5%:	Pred. No. 2.6e-82:	
Matches 421:	Conservative 0:	Mismatches 1:	Indels 1: Gaps 1:
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QY	69	GGCCAAGGCGGCACCTCGTAGCCCCAGGTGTGACTGTCCCGTGAATTCCAAAGAAGAT	128
Db	61	GGCCAAGGCGGCACCTCGTAGCCCCAGGTGTGACTGTCCCGTGAATTCCAAAGAAGAT	120
QY	129	TGCTGTGTTTTGTGCAAGAGCGTGGCCAGCGGGGCGACACTGAAAGCCCTTGACAGGA	188
Db	121	TGCTGTGTTTTGTGCAAGAGCGTGGCCAGCGGGGCGACACTGAAAGCCCTTGACAGGA	180
QY	189	GCCGCGGCGCAACTCACCTGCTGTGTGTCGCCCAAGAACCTTGGCGCTGGGAGAA	248
Db	181	GCCGCGGCGCAACTCACCTGCTGTGTGTCGCCCAAGAACCTTGTGGCGCTGGGAGAA	240

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OY	309	GCTGGAGAAGCTGTTGACGATGTGGCCACACCCTGTGCTGAAGCAGAGTGGTTGT	368
Db	301	GCTGGAGAAGCTGTTGACGATGTGGCCACACCCTGTGCTGAAGCAGAGTGGTTG -	359
OY	369	GGAGTGCACAGGTACGCCAATGTGTGACAGCTTACCTTGTACTGCCAACATGCTTAG	428
Db	360	GGAGTGCACAGGTACGCCAATGTGTGACAGCTTACCTTGTACTGCCAACATGCTTAG	419
OY	429	CTG 431	
Db	420	CTG 422	
RESULT	9		
LOCUS	H41522	433 bp mRNA	EST 31-JUL-1995
DEFINITION	YN90F12.s1 Soares adult brain N2B5HB55Y Homo sapiens cDNA clone IMAGE:175727 3', mRNA sequence.		
ACCESSION	H41522		
VERSION	H41522.1 GI:917574		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 433) Hillier,L., Clark,N., Dubnue,T., Elliston,R., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterson,R., Williamson,A., Woldmann,P. and Wilson,R. The WashU-Merck EST Project Unpublished (1995) On Dec 20, 1995 this sequence version replaced gi:1134270. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu Insert Size: 852 High quality sequence stops: 360 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. Insert Length: 852 Std Error: 0.00 Seq primer: Promega -21ml3 High quality sequence stop: 360.		
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COMMENT			
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	/sex="Male"		
	/dev_stage="55-year old"		
	/lab_host="DH10B (ampicillin resistant)"		
	/note="Organ: brain; Vector: pRT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - Oligo(dT) primer [5' TGTTACCAATCTGAAAGTGGAGCGCGCGCGCTTTTTTTTTTTTTTTT 3'] , digested with Not I and Eco RI sites of a modified pRT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was		



VERSION	AI81528.1	GI:5398094
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .	
AUTHORS	1 (bases 1 to 623)	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	
	Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	On Oct 6, 1998 this sequence version replaced gi:3709744.	
	Contact: Robert Strausberg, Ph.D.	
	Email: Robert_Strausberg@nih.gov	
	Tel: (301) 496-1550	
	Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.	
	Emmert-Buck, M.D., Ph.D.	
	CDNA Library Preparation: Life Technologies, Inc.	
	CDNA Library Arrayed by: Greg Lennon, Ph.D.	
	DNA Sequencing by: Washington University Genome Sequencing Center	
	Clone distribution: NCI-CGAP clone distribution information can be	
	found through the I.M.A.G.E. Consortium/LLNW, at:	
	<a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a>	
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ORIGIN		
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Matches 333; Conservative	0; Mismatches 14; Indels 0; Gaps 0;	
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Db	622 TGCCAGCAGAGACTTTGGCCCCGCTGCTGCGCCACACTCTGCGCAGAGTCCCGAGCGG 563	
QY	968 GCTGCGCAGCATATGCTGACAGCCGGGCCCGGACACTTACGAGCTGATGACGGGGTCC 1027	
Db	562 CTCGCCAGCATATGCTGACAGCCGGGCCCGGACACTTACGAGCTGATGACGGGGTCC 503	
QY	1028 CAGCGCGCGCTGAGAGAGTTCGTGCGCCAGCGTGGGCTGCGCAGAGCAGAGATCGAAG 1087	
Db	502 CAGCGCGCGCTGAGAGAGTTCGTGCGCCAGCGTGGGCTGCGCAGAGCAGAGATCGAAG 443	
QY	1088 CCGTGAGAGTGAGATCGGCGCTTCCGAGACACAGCATAGAGATGCTCAAGCGCTTGC 1147	
Db	442 CCGTGAGAGTGAGATCGGCGCTTCCGAGACACAGCATAGAGATGCTCAAGCGCTTGC 383	
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Db	382 GCCAGACAGACCCCGGGGGCTCTGGAGAGCGCTTTACGGGGCTCTGGAGCGCATGGGGCTGG 323	
QY	1208 ACGGCTGGTGAAGACTTGGCAGACCCCTGACAGCGCGGCGCGTGA 1254	
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[illegible]

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LOCUS			
DEFINITION	AA934992		
ACCESSION	AA934992	345 bp	mRNA
VERSION	AA934992.1	GI:3092204	EST
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 345)		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
COMMENT	Unpublished (1997)		
	On Apr 21, 1998 this sequence version replaced gi:3072128.		
	Contact: Robert Strausberg, Ph.D.		
	Tel: (301) 496-1550		
	Email: Robert.Strausberg@nih.gov		
	This clone is available royalty-free through LINDL; contact the IMAGE Consortium (info@image.lindl.gov) for further information.		
	Insert Length: 1648 Std Error: 0.00		
	Seq primer: -40m13 fwd. ET from Amersham		
	High quality sequence stop: 131.		
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	/db_xref="taxon:9606"		
	/clone="IMAGE:1578681"		
	/clone_lib="Soares_NFL_T_GBC_S1"		
	/lab_host="DH10B"		
	/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NH7, and B-cell NCI-GAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as template in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldi."		
BASE COUNT	56 a	105 c	116 g
ORIGIN		68 t	
Query Match	23.1%;	Score 289.6;	DB 33; Length 345;
Best Local Similarity	96.6%;	Pred. No.2.2e-55;	
Matches 317; Conservative	0;	Mismatches 9;	Indels 2;
		Gaps 2;	
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QY	148	GGCTGGCCAGCGGGGACATGACCTGGAAGGCCCTTGAGGAGAGCGCCGGGCAACTCCACC	207
Db	133	GGGTGGCCAGCGGGGACATGACCTGGAAGAGCCCTTGAGGAGAGCGCGGACACTCCACC	192

[illegible]

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Db 587 ACACCTTTGGCAGAGATCCAGGCGGGCTGCGAAGCCATGATGTGCAAGCGGCGCCGAC 528
OY 1003 CTTTACGAGCTATGAGCCGGTCCAGCGCGCGTGTGAAGAGTTCGTGGCAGCGTG 1062
Db 527 CTTTACGAGCTATGAGCCGGTCCAGCGGCGCGTGTGAAGAGTTCGTGGCAGCGTG 468
OY 1063 GGGCTGCGCGAGAGATCGAAGCCGCTGAGGTGAGATCGGCGCTTCGAGACCGAG 1122
Db 467 GGGCTGCGCGAGAGATCGAAGCCGCTGAGGTGAGATCGGCGCTTCGAGACCGAG 408
OY 1123 CAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACCGCGCGCTCGAGAGCGTTTAC 1182
Db 407 CAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGACCGCGCGCTCGAGAGCGTTTAC 348
OY 1183 GCGGCGCTGAGAGCGCTGAGCGCTGTGACCGCTGCTGTGAAGACTTGGCAGCGCTTAC 1242
Db 347 GCGGCGCTGAGAGCGCTGAGCGCTGTGACCGCTGCTGTGAAGACTTGGCAGCGCTTAC 288
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Db 287 CCGGCGCGCTGA 276

RESULT 15
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LOCUS zdb6a06.r1 Soares_fetal_heart_Nbhlh19w Homo sapiens cDNA clone
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ACCESSION W76376
VERSION W76376.1 GI:1386600
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
On Jan 7, 1998 this sequence version replaced gi:948013.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 850L, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 969 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 352.
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/sex="unknown"
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/note="Organ: heart; Vector: pT73p (Pharmacia) with a
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strand cDNA was primed with a Not I - oligo(dT) primer [5'
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double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of

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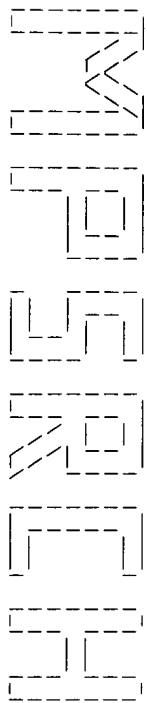
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normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetus as the fetal lung library, Soares fetal lung
Nbhlh19w.
BASE COUNT 71 a 133 c 106 g 59 t 3 others
ORIGIN
Query Match 21.8%; Score 273.2; DB 91; Length 372;
Best Local Similarity 96.3%; Pred. No. 1,1e-51;
Matches 342; Conservative 0; Mismatches 6; Indels 7; Gaps 6;
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OY 755 TGTACACCTTGGAGACGCGCCACACCCCTTGTAGACCTCTGACAGCAGTGAAGATCT 814
Db 67 TGTACACCTTGGAGACGCGCCACACCCCTTGTAGACCTCTGACAGCAGTGAAGATCT 126
OY 815 GCACCGTCCAGTTGGTGGTAACAGCTGAGACCCCTGGCTACCCGAGACCCGAGGCGC 874
Db 127 GCACCGTCCAGTTGGTGGTAACAGCTGAGACCCCTGGCTACCCGAGACCCGAGGCGC 186
OY 875 TCTGCGCGGAGTGAATGGTCCCTGGAGACAGTTGCCAGAGAGCTTGGCCCGCTG 934
Db 187 TCTG-CGCGANGTGATGCTGTGGG-CAGTTGCCAGAGAGA-NTCTTGGCCCGCTG 243
OY 935 CTGGGCCACACCTCTGCCAGAGTCCCGAGCGGCTGCGCAGCCA--TGATGCTCAGCC 992
Db 244 CTGGGCCACACCTCTGCCAGAGTCCCGAGCGGCTGCGCAGCCAATGANTGCTGACCC 303
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Search completed: July 23, 2000, 06:13:02  
Job time: 4247 sec

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Distribution rights by Oxford Molecular Ltd

Msrch\_PP protein - protein database search, using Smith-Waterman algorithm  
Run on: Tue Jul 25 22:22:14 2000; Maspar time 13.99 Seconds  
724.413 Million cell updates/sec  
Tabular output not generated.

Title: >US-09-314-889-2  
Description: (1-428) from US09314889.pep  
Perfect Score: 3267  
Sequence: 1 MEETQCGEARQGRLRGESAA.....ERMGLDCVEDLRSLRQGP 428

Scoring table:  
PAM 150  
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq36  
1:geneseqp

Statistics: Mean 35.731; Variance 153.828; scale 0.232

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	3267	100.0	428	W31516	Death domain containin	0.00e+00
2	3267	100.0	428	W95537	Death domain containin	0.00e+00
3	3118	95.4	417	W31517	Death domain containin	4.51e-293
4	3118	95.4	417	W26709	Human apoptosis protei	4.51e-293
5	3118	95.4	417	W95538	Death domain containin	4.51e-293
6	3118	95.4	417	W57045	Human apoptosis induci	4.51e-293
7	3118	95.4	833	W64486	Human DR3 protein.	4.51e-293
8	1962	60.1	411	W57046	Mouse apoptosis induci	6.35e-178
9	1342	41.1	181	W26708	Human apoptosis protei	1.40e-116
10	503	15.4	65	W93610	Human Fas protein frag	4.88e-35
11	412	12.6	909	W64485	Human DR3 protein frag	1.74e-26
12	408	12.5	455	R07451	Human TNF receptor	4.12e-26
13	407	12.5	455	R10986	30KD TNF inhibitor pre	5.10e-26
14	407	12.5	455	R75084	p55 TNF-R.	5.10e-26
15	407	12.5	455	R42059	Lambda derived TNF-R.	5.10e-26
16	404	12.4	455	R12082	Human 55KD TNF-binding	9.71e-26
17	400	12.4	443	R20787	TNF-alpha binding prot	2.29e-25
18	400	12.2	443	R51033	Mutant p55 tumour necr	2.29e-25
19	400	12.2	455	R51034	Mutant p55 tumour necr	2.29e-25
20	400	12.2	455	R42197	p55 Tumour necrosis fa	2.29e-25
21	394	12.1	455	R12550	Type I TNF receptor.	8.27e-25
22	387	11.8	433	R51032	Mutant p55 tumour necr	3.69e-24
23	372	11.4	455	R24000	TNF-alpha 55KD recepto	9.05e-23

ALIGNMENTS

24	351	10.7	461	1	R07450	Rat Tumour Necrosis Fa	7.82e-12
25	271	8.3	256	1	W33357	TBP(20-161)/hCG-alpha	1.43e-13
26	248	7.6	336	1	W33360	TBP(20-190)/hCG-beta	1.58e-11
27	245	7.5	108	1	W73570	Cytoplasmic domain of	2.91e-11
28	246	7.5	199	1	R24080	Truncated TNF-alpha 55	2.38e-11
29	246	7.5	211	1	W89225	Tumour necrosis factor	2.38e-11
30	245	7.5	285	1	W33359	TBP(20-190)/hCG-alpha	2.91e-11
31	246	7.5	307	1	W33358	TBP(20-161)/hCG-beta	2.38e-11
32	246	7.5	309	1	R70108	TNF-R-GBPH fusion prot	2.38e-11
33	246	7.5	311	1	W89229	Tumour necrosis factor	2.38e-11
34	246	7.5	366	1	W89228	Tumour necrosis factor	2.38e-11
35	246	7.5	371	1	R07449	Tumour Necrosis Factor	2.38e-11
36	246	7.5	397	1	W89227	Tumour necrosis factor	2.38e-11
37	246	7.5	417	1	W89226	Tumour necrosis factor	2.38e-11
38	246	7.5	420	1	W89224	Tumour necrosis factor	2.38e-11
39	246	7.5	451	1	R70107	TNF-R-GBP 130 fusion p	2.38e-11
40	246	7.5	547	1	R70104	TNF-R-GBPH fusion prot	2.38e-11
41	246	7.5	900	1	R70103	TNF-R-GBP 130 fusion p	2.38e-11
42	246	7.5	1245	1	R70106	TNF-R-Pl. vivax Duffy	2.38e-11
43	246	7.5	1604	1	R70105	TNF-R-EBA 175 fusion p	2.38e-11
44	243	7.4	884	1	R70109	TNF-R-GBP 130 fusion p	4.37e-11
45	240	7.3	161	1	R27496	Native 30 kD TNF inh	8.03e-11

ALIGNMENTS

RESULT	1	
ID	W31516	standard; Protein; 428 AA.
AC	W31516;	
DT	02-MAR-1998	(first entry)
DE	Death domain containing receptor DR3-VI.	
KW	Death domain containing receptor; DR3-VI; human; apoptosis; inflammation; NF-kappaB.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Peptide	1..35
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FT	Domain	/note="extracellular domain"
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FT	Domain	/note="transmembrane domain"
FT	Domain	236..428
FT	Domain	/note="intracellular domain"
FT	Domain	353..419
FT	Domain	/note="death domain"
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PN	W09733904-A1.	
PD	18-SEP-1997.	
PF	17-OCT-1996; U16849.	
PR	12-MAR-1996; US-013285.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(UNMI) UNIV MICHIGAN.	
PI	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;	
DR	WFI: 97-470812/43.	
DR	N-PSDB: T89426.	
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-VI	
PT	for activation of apoptosis and NF-kappaB, antagonists can be used	
PT	to treat inflammatory diseases	

PS Claim 1: Page 71-73: 108pp: English.  
 CC This protein comprises human death domain containing receptor  
 CC DR3-V1, a novel member of the tumour necrosis factor receptor  
 CC family. Its amino acid sequence was deduced from a cDNA clone  
 CC (see T89426) isolated from a human testis tumour library. Related  
 CC death domain containing receptor DR3 (see W31517) has also been  
 CC identified. Recombinant full-length or mature DR3-V1 can be  
 CC expressed in transformed host cells. These polypeptides can be  
 CC used to treat diseases and disorders associated with the inhibition  
 CC of apoptosis, or to screen for modulator compounds. Antagonists,  
 CC such as antibodies raised against DR3-V1, can be used to treat  
 CC diseases and disorders associated with increased apoptosis and for  
 CC treating inflammatory diseases and disorders.  
 SQ Sequence 428 AA;

Query Match 100.0%; Score 3267; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MEETQGEAPRGQLRGSSAARVPQALLVLLGARAQGTSPRCDCAGDFHKKIGLFCR 60
QY      1 MEETQGEAPRGQLRGSSAARVPQALLVLLGARAQGTSPRCDCAGDFHKKIGLFCR 60
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Db      61 GCPAGHYLKAPCTEPCGNSSTCLVCPDPTFLAMENHNSECARQACDQASQVALENC 120
QY      61 GCPAGHYLKAPCTEPCGNSSTCLVCPDPTFLAMENHNSECARQACDQASQVALENC 120
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Db      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
QY      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
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QY      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
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QY      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
        |||
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QY      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
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QY      241 HKPLVTADGAGMEALTPPATHTLSPLDSAHNTLLAPDSESEKICTVQLVGNSWTPGYPTQ 300
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QY      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
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QY      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
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Db      361 FVRTGLREAEIEAVEVEIGFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVE 420
QY      361 FVRTGLREAEIEAVEVEIGFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVE 420
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Db      421 RSRLQGRG 428
QY      421 RSRLQGRG 428

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RESULT 2  
 ID W95537 standard; Protein; 428 AA.  
 AC W95537;  
 DT 25-MAR-1999 (first entry)  
 DE Death domain containing receptor polypeptide (DR3-V1).  
 KW Death domain; receptor; DR3-V1; DR3; recombinant.  
 OS Homo sapiens.  
 FH Key  
 FT Peptide 1..35  
 FT /note= "signal peptide"  
 FT Protein 36..428  
 FT /note= "mature protein"  
 PN J11000170-A.  
 PD 06-JAN-1999.  
 PE 12-MAR-1997; 057503.  
 PR 06-FEB-1997; US-037341.  
 PR 12-MAR-1996; US-013285.  
 PR 17-OCT-1996; US-028711.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (UNMT) UNIV MICHIGAN.  
 PR WPI; 99-124390/11.

DR N-PSDB: X00924.  
 PT New death domain containing receptor and recombinant vector -  
 PT optionally comprising leader sequence  
 PS Claim 1; Fig 1, 2; 50pp: Japanese.  
 CC The invention provides nucleotide sequences encoding death domain  
 CC containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone  
 CC is contained in ATCC deposition No. 97456 and the DR3 cDNA clone is  
 CC contained in ATCC deposition No. 97757. Recombinant vectors comprising  
 CC for the nucleic acid sequences and optionally the leader sequences are used  
 CC for the recombinant production of the proteins. The present sequence  
 CC represents the amino acid sequence of a death domain containing receptor  
 CC polypeptide (DR3-V1).  
 SQ Sequence 428 AA;

Query Match 100.0%; Score 3267; DB 1; Length 428;  
 Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
 Matches 428; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MEETQGEAPRGQLRGSSAARVPQALLVLLGARAQGTSPRCDCAGDFHKKIGLFCR 60
QY      1 MEETQGEAPRGQLRGSSAARVPQALLVLLGARAQGTSPRCDCAGDFHKKIGLFCR 60
        |||
Db      61 GCPAGHYLKAPCTEPCGNSSTCLVCPDPTFLAMENHNSECARQACDQASQVALENC 120
QY      61 GCPAGHYLKAPCTEPCGNSSTCLVCPDPTFLAMENHNSECARQACDQASQVALENC 120
        |||
Db      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
QY      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
        |||
Db      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
QY      121 VADTRCGCKPGWFEVCQVSSSPFYCOPCLDGCALHRRHRLCSRRTDCGCLPGF 180
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Db      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
QY      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
        |||
Db      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
QY      181 YEHGDCVSCPTSTLGSCEPCAAVCGWRQMFVQVLLAGLVPLLLGATLTYTYRHCP 240
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Db      241 HKPLVTADGAGMEALTPPATHTLSPLDSAHNTLLAPDSESEKICTVQLVGNSWTPGYPTQ 300
QY      241 HKPLVTADGAGMEALTPPATHTLSPLDSAHNTLLAPDSESEKICTVQLVGNSWTPGYPTQ 300
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Db      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
QY      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
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Db      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
QY      301 EALCPQVWMSMDQLPSRALGPAAPTLSPESPAGSAMMLQGPOLYDVMADVAPARRWKE 360
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Db      361 FVRTGLREAEIEAVEVEIGFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVE 420
QY      361 FVRTGLREAEIEAVEVEIGFRDQOYEMLKRWROQOPAGLGAVYAALERMGLDGCVE 420
        |||
Db      421 RSRLQGRG 428
QY      421 RSRLQGRG 428

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RESULT 3  
 ID W31517 standard; Protein; 417 AA.  
 AC W31517;  
 DT 02-MAR-1998 (first entry)  
 DE Death domain containing receptor DR3.  
 KW Death domain containing receptor; DR3-V1; human; apoptosis;  
 KW inflammation; NF-kappaB.  
 OS Homo sapiens.  
 FH Key  
 FT Peptide 1..24  
 FT /label= Sig\_peptide  
 FT Domain 25-201  
 FT /note= "extracellular domain"  
 FT Domain 202..224  
 FT /note= "transmembrane domain"  
 FT Domain 225..417  
 FT /note= "intracellular domain"  
 FT Domain 342..408  
 FT /note= "death domain"  
 PN W09733904-A1.  
 PD 18-SEP-1997.  
 PR 17-OCT-1996; U16849.



Query Match	95.4%;	Score 3118;	DB 1;	Length 417;
Best Local Similarity	98.3%;	Pred. No. 4,51e-293;		
Matches 407;	Conservative 3;	Mismatches 4;	Indels 0;	Gaps 0;

FT	Domain	/note= "intracellular domain"
FT		338..417
FT	Modified_site	/note= "death domain"
FT		67
FT	Modified_site	/note= "N-glycosylated"
FT		106
FT		/note= "N-glycosylated"
PM	WO9737020-A1.	
PD	09-OCT-1997.	
PF	31-MAR-1997.	U05230.
PR	23-SEP-1996.	US-710802.
PR	01-APR-1996.	US-625328.
PA	(GENE )	GENENTECH INC.
PI	Ashkenazi Aj.	
DR	WPI: 97-503105/46.	
DR	N-PSDB: 791180.	
PT	Polyptide(s) Apo-3 and Apo-2L1 -	useful for regulating apoptosis
PS	in mammalian cells	
PS	Claim 19: Page 46-48; 70pp: English.	
CC	This novel polypeptide, designated Apo-3, is a protein that	
CC	stimulates or induces apoptotic activity in mammalian cells	
CC	purposes. Its amino acid sequence was deduced from a human foetal	
CC	heart cDNA clone (see T91180). The N-terminal 181 amino acids of	
CC	Apo-3 are identical to the sequence of another novel apoptotic	
CC	polypeptide, Apo-2L1 (see W26709). Also claimed are: chimeric	
CC	comprising the extracellular or death domain of Apo-3; chimeric	
CC	molecules comprising Apo-3 fused to a heterologous amino acid	
CC	sequence; antibodies that bind to Apo-3 or its extracellular	
CC	domain; nucleic acids encoding the polypeptides, as well as	
CC	vectors and host cells; a non-human transgenic animal containing	
CC	cells that express nucleic acid encoding Apo-3; and a non-human	
CC	knockout animal containing cells having an altered Apo-3 gene.	
CC	Apo-3 can be used to induce apoptosis or NF-kappa-B (NF-kB) - or	
CC	JNK-mediated gene expression for therapeutic purposes. Apo-3-196	
CC	fusion proteins can be used to inhibit apoptosis or NF-kB	
CC	induction or JNK activation for therapeutic purposes, and can	
CC	be used as immunogens for anti-Apo-3 antibody production.	
CC	Apo-3 or Apo-2L1 can also be used as assay standards. The	
CC	animals can be used in drug screening and development.	
SO	Sequence 417 AA;	
	Query Match	95.4%; Score 3118; DB 1; Length 417;
	Best Local Similarity	98.3%; Pred. No. 4 Site-293;
	Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
Db	4 RPRGCAAAVAAALLLVILGARAAGGTSPDRCCADDFKKIGLFFCCRCGRPHYKACCTE	63
Oy	15 RGSAAAPVQALLVILGARAAGGTSPDRCCADDFKKIGLFFCCRCGRPHYKACCTE	74
Db	64 PCGNSTCLVCQDPTFLAENHNHSECAQCAQDAQSOVALENCASAVADTRCGCKPGMFV	123
Oy	75 PCGNSTCLVCQDPTFLAENHNHSECAQCAQDAQSOVALENCASAVADTRCGCKPGMFV	134
Db	124 ECGYSQCVSSSPFFCQCPQLDCGALHNRTRILCSNRPTDCGLPFGFHEHSDGCVSCTST	183
Oy	135 ECGYSQCVSSSPFFCQCPQLDCGALHNRTRILCSNRPTDCGLPFGFHEHSDGCVSCTST	194
Db	184 LGSCEPCAAACGMRQMFVQVLLAGLVLPPLLCATLTYYYRHQWPKPLVTADAEAMEA	243
Oy	195 LGSCEPCAAACGMRQMFVQVLLAGLVLPPLLCATLTYYYRHQWPKPLVTADAEAMEA	254
Db	244 LTPPPATHLSPLDSANHLAPRDSSEKICVYOLVGNSTWTEGYPETQALCPDYTWSDOL	303
Oy	255 LTPPPATHLSPLDSANHLAPRDSSEKICVYOLVGNSTWTEGYPETQALCPDYTWSDOL	314
Db	304 PSRALGPAAPATLTSPSPAGSPAMMLCPGPLYVMVAVARPKKEVRLTGLREARTEA	363
Oy	315 PSRALGPAAPATLTSPSPAGSPAMMLCPGPLYVMVAVARPKKEVRLTGLREARTEA	374
Db	364 VEVEIGRPDOQYEMLRKRWQOPAGIGAYVALERMGLDGCVEDLSRLQORQ	417
Oy	375 VEVEIGRPDOQYEMLRKRWQOPAGIGAYVALERMGLDGCVEDLSRLQORQ	428



PR 28-JAN-1997; US-035722.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI (UNMI) UNIV MICHIGAN.  
 PI Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;  
 DR WPI: 98-427952/36.  
 PT Nucleic acid encoding human death domain-containing receptor 4 -  
 PT useful for therapeutic modulation of apoptosis, in e.g. cancer and  
 PT autoimmune diseases  
 PS Disclosure: Fig 2: 92pp: English.  
 CC This sequence represents the human death domain containing receptor-3  
 CC DR3 which is used in a method resulting in the isolation of a human death  
 CC domain containing receptor 4, DR4. DR4 agonists are used to increase  
 CC apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in  
 CC cases of cancer, autoimmune disease, viral or other infections,  
 CC inflammation, graft vs. host disease, acute or chronic graft rejection,  
 CC Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of  
 CC acquired immune deficiency syndrome, neurodegenerative disease,  
 CC myelodysplastic syndrome, ischemic injury, toxin-induced liver damage,  
 CC septic shock, cachexia and anorexia, also a wide range of inflammatory  
 CC conditions. DR4 fragments of the protein are used diagnostically, e.g.  
 CC to detect mutant forms of DR4 (possibly associated with disease), for  
 CC isolating the DR4 gene or related sequences and for chromosomal mapping.  
 SQ Sequence 833 AA;

Query Match 95.4%; Score 3118; DB 1; Length 833;  
 Best Local Similarity 98.3%; Pred. No. 4 51e-293;  
 Matches 407; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAPCTE 63  
 15 RGESAPVPQALLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAPCTE 74  
 Db 64 PCGNSTCLVCPQDFFLAENHHNSCARQACDEQASVALNCSAVATRCGCKRGWV 123  
 75 PCGNSTCLVCPQDFFLAENHHNSCARQACDEQASVALNCSAVATRCGCKRGWV 134  
 Db 124 ECVQSCVSSSPFYCQPLDGCALHRRHRLCSRRDTCGTLPGFYEHDGCVSCPTST 183  
 135 ECVQSCVSSSPFYCQPLDGCALHRRHRLCSRRDTCGTLPGFYEHDGCVSCPTST 194  
 Db 184 LGSCPERCAAVGMRQMFVVOYLLAGLVPLLLGATLTYYTRHCHWPKPLVTADGAGMA 243  
 195 LGSCPERCAAVGMRQMFVVOYLLAGLVPLLLGATLTYYTRHCHWPKPLVTADGAGMA 254  
 Db 244 LTPPATHTLSPDLSAHTLLAPDSSEKICTYQLVGNSWTPGYPTQDALCPQVTWSMDL 303  
 255 LTPPATHTLSPDLSAHTLLAPDSSEKICTYQLVGNSWTPGYPTQDALCPQVTWSMDL 314  
 Db 304 PSRALGPAAAPTLSPEPAGSPAMMLQPPOLYDVMDAVPARMKKEFVTLGLREAETEA 363  
 315 PSRALGPAAAPTLSPEPAGSPAMMLQPPOLYDVMDAVPARMKKEFVTLGLREAETEA 374  
 Db 364 VEVEIGRFDOQYEMLKRMROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 417  
 375 VEVEIGRFDOQYEMLKRMROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 428

RESULT 8  
 ID W57046 standard; Protein; 411 AA.  
 AC W57046;  
 DT 20-AUG-1998 (first entry)  
 DE Mouse apoptosis inducing receptor.  
 KW Apoptosis inducing receptor; AIR protein; mouse; cell death regulator;  
 KM Type I transmembrane protein; tumour cell death; autoimmune disease;  
 therapy.  
 OS Mus sp.  
 PN MO9814565-A1.  
 PD 09-APR-1998.  
 PF 03-OCT-1997; U17876.  
 PR 04-OCT-1996; US-044456.  
 PA (IMMV) IMMUNEX CORP.  
 PI Perkins PA;  
 DR WPI: 98-240077/21.

DR N-PSDB: V28701.  
 PT DNA encoding apoptosis inducing receptor - which is Type I  
 PT transmembrane protein, useful for regulating cell death  
 PS Claim 16; Page 33-35; 45pp; English.  
 CC This sequence is the mouse apoptosis inducing receptor (AIR) of the  
 CC invention. AIR is a Type I transmembrane protein, soluble forms of which  
 CC can be used to regulate cell death in a therapeutic setting. Soluble AIR  
 CC can also be used in vitro to block apoptosis or AIR-expressing cells, or  
 CC to screen agonists or antagonists of AIR activity. The cytoplasmic domain  
 CC of AIR can be used to develop assays for inhibitors of AIR-induced cell  
 CC death, which is useful to regulate cell death in a therapeutic setting as  
 CC well as in vitro. Agonists of AIR activity can be used to kill tumour  
 CC cells that express AIR, or T cells expressing AIR in autoimmune diseases.  
 SQ Sequence 411 AA;

Query Match 60.1%; Score 1962; DB 1; Length 411;  
 Best Local Similarity 65.9%; Pred. No. 6.35e-178;  
 Matches 267; Conservative 61; Mismatches 61; Indels 16; Gaps 9;

Db 21 LLLLLLGGGCGGM-SGRCCASSESKRYGPFCCRCGPKHMKAPCAEPCCNSTCLPCP 79  
 26 LLLVLLGARAAGGTRSPRCDCAGDFHKKIGLFCRCGPAGHYLKAPCTEPCGNSTCLVCP 85  
 Db 80 SDFTFLTRDNHFKTDCTRCQYCDDEALQVTLNCSAKSDTRCGCGSGWCYDCSTPCGKSS 139  
 86 QDFFLAENHHNSCARQACDEQASVALNCSAVATRCGCKRGFVECVQSCVSS 145  
 Db 140 PFCSCVPGATTPVH-EAP---TPR----PCLDFYIRGNDCTSCPTGFSSVCRACTAV 190  
 146 PFYCPQLDGCALHRRHRLCSRRDTCGTLPGFYEHDGCVSCPTSTLGSCPERCAAV 205  
 Db 191 CGKRMQMFVVOYLL-G--VALFLGALLCAVCR-WQPKAVVYVADTATETFLASQTHTLS 246  
 206 CGKRMQMFVVOYLLAGLVPLLLGATLTYYTRHCHWPKPLVTADGAGMALTPPATHTLS 264  
 Db 247 ASDSAHTLLAPSSSTGKICTYQLVGNMNTPGLSQTQEVVCGQASQPMDDLPNRTLTGPTL 306  
 265 PLDSAHTLLAPSSSEKICTYQLVGNSWTPGYPTQDALCPQVTWSMDLPSALGPAA 323  
 Db 307 ASPLSPAPAGSPAAVLOPPOLYDVMDAVPARMKKEFVTLGLREAIEAVEVEIGRF 366  
 324 APTLSPEPAGSPAMMLQPPOLYDVMDAVPARMKKEFVTLGLREAIEAVEVEIGRF 383  
 Db 367 DOQYEMLKRMROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 411  
 384 DOQYEMLKRMROQOPAGLGAVVAALERMGLDGCVEDLRSRLQGRP 428

RESULT 9  
 ID W26708 standard; Protein; 181 AA.  
 AC W26708;  
 DT 14-APR-1998 (first entry)  
 DE Human apoptosis protein Apo-2LI.  
 KW Apo-2LI; apoptosis; Apo-2 ligand inhibitor; human; therapy.  
 OS Homo sapiens.  
 FH key Location/Qualifiers  
 FT Peptide 1..20  
 FT Modified\_site 67 /label= sig\_peptide  
 FT FT /note= "N-glycosylated"  
 FT Modified\_site 106 /note= "N-glycosylated"  
 PN WO9737020-A1.  
 PD 09-OCT-1997.  
 PF 31-MAR-1997; U05230.  
 PR 23-SEP-1996; US-710802.  
 PR 01-APR-1996; US-625328.  
 PA (GERTH) GENENTECH INC.  
 PI Ashkenazi AJ;  
 DR WPI: 97-503105/46.  
 DR N-PSDB: T91179.  
 PT Polyptide(s) Apo-3 and Apo-2LI - useful for regulating apoptosis  
 PT in mammalian cells



Df	375	RULSDHEIDRLDLONGCLAEAOYSLMATHRRRTPREATLLELLGKVLDRMDLGLED	434
Oy	364	TGLEAEALIEAVEVEIGR-FRDQOYEMLKRWRDOP--AGLAGVAVALERMGJGDGED	419
Df	435	IIEAL 439	
Oy	420	LRSRL 424	
<hr/>			
RESULT	12		
ID	R07451 standard; protein; 455 AA.		
AC	R07451:		
DT	29-JAN-1991 (first entry)		
DE	Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.		
KW	Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;		
KW	Infectious disease; parasitic disease; cachexia;		
KW	autoimmune disease; shock; lambdaTNF-R2; ratNF-R8,		
OS	Homo sapiens.		
PN	EP-393438-A.		
PD	24-OCT-1990.		
PF	06-APR-1990; 106624.		
PR	21-APR-1989; DE-913101.		
PR	21-JUN-1989; DE-920282.		
PA	(BOEH ) BOEHRINGER INGELHEIMINT.		
P1	Hauptmann R, Himmeler A, Maurer-Poyg I, Stratowa C;		
DR	MPLr: 90-321987/43.		
DR	N-PSDB: Q06285.		
PT	DNA encoding TNF binding protein and TNF-receptor - used in		
PT	tumour treatment and to understand mechanismism to TNF action		
PS	Disclosure: Fig 9(1-2); 51pp; German.		
CC	ratiNF-R8 (Q06284) was used to screen the HS913T cDNA library.		
CC	lambdaTNF-R2 encodes the complete human TNF-R2 and was used to		
CC	construct a plasmid (padTNF-R) expressing the product the same way		
CC	as pADTNF-BP (see Q06282). The expressed proteins are useful		
CC	physiolactically and therapeutically to control disorders which		
CC	involve the damaging effects of TNF-alpha or -beta (e.g. infectious or		
CC	parasitic diseases, shock, cachexia, autoimmune diseases, adult		
CC	respiratory distress syndrome etc., or side effects of treatment with		
CC	TNF-alpha). They can also be used as diagnostic reagents for		
CC	assaying TNF and in study of TNF-receptor interactions.		
CC	See also Q06282-Q06285.		
SQ	Sequence 455 AA;		
<hr/>			
Query Match	12.5%;	Score 408;	DB 1; Length 455;
Best Local Similarity	29.9%;	Pred. No. 4,12e-26;	
Matches 127;	Conservative 81;	Mismatches 177;	Indels 40; Gaps 32;
Df	27	VIGLVPHLDGEKRDYSVCPGGTYITHPONNISICTKCHKGTLYINDCGPGODTDRCRES	86
: :	:	:	:
Oy	30	LLGARAGGGTRSPR-CDDA-GDF-HKKIGILGFCCGCAGHYTLAKPCREPGNSTGLVCPO	86
Df	87	GSPFLASENHLR-NCLSSCKRKEMGOVEIISCTVDRTFYGCCRKNOYRIHW-SENLFQC-	143
: :	:	:	:
Oy	87	DTEFLAMENHNHSEDCARCOADCDSQVALENCNSAVADRGCGRGVMEQVSQCVSSSP	146
Df	144	FNCSELICN-GNVH---LSCOEKONTYC-NCHAGPEFLRENEGYSCSKCKSLECTKIQLP	197
: :	:	:	:
Oy	147	FYCQPCILDCAHLNHTKLIC-SRNDTCGCTLCRFETFGDGCVSCPSTYLG-SCPERC-A	203
Df	198	QIQNWKTEDSGTVLLP-LVFIFGLCILSLFTGLMYRYQRMSKLYSIYCSKPSTEKE	256
: :	:	:	:
Oy	204	AVCGMROMF-W-VQVILLAGLVV--PL-LTGATILT-YTHR-HCMPHK--PLVTADAEN-GME	253
Df	257	GELEGTTTKPLARPDSPPRPGRPTLTGFPVBSSTTSSTYTTPGDCPFAPAAREVPAR	316
: :	:	:	:
Oy	254	A-LTPPATHTLSPUDS-AHTL-LAPPSSSKICTIVOLVGNS-WTPGVPEHQEALCPDYT-	308
Df	317	PYOAGADITLATASDP-IIPNPLOKWEDSAKHPQSOLDTDPATLYAAVENPYLRMKEFVR	376
: :	:	:	:
Oy	309	-W-SMODLPBRALCPAAPPI-LSP-EESPASSPMAMDLPQGO-LYDVWDAYPARWKKEFVR	363
Df	377	RGLGSDEHDRLDELONCRCLREAOYSLMATWRRRTPREATLLELLGKVLDRMDLGLED	436

QY	364	TLGLREAIIEAVEVEIGR-FRDQGYEMLKRRRQGP---	AGLGAVYALALERMGLDGCVED	419
Db	437	IEEAL 441		
OY	420	LR SRL 424		
RESULT	13			
ID	R10986	standard; Protein; 455 AA.		
AC	R10986;			
DT	13-MAY-1991	(first entry)		
DE	30kD TNF inhibitor precursor.			
KM	Tumour necrosis factor; inhibitor.			
OS	Homo sapiens.			
FM	Key	Location/Qualifiers		
FT	cleavage_site	40..41		
PT	note=" cleavage gives active protein "			
PD	AU058976-A.			
PD	24-JAN-1991.			
PR	16-JUL-1990; 058976.			
PR	18-JUL-1989; US-381080.			
PR	11-DEC-1989; US-450329.			
PR	07-FEB-1990; US-479661.			
PA	(SYNTE-) STERGEN INC.			
DR	WPI; 91-073847/11.			
DR	N-PSDB; Q10883.			
PT	Tumour necrosis factor inhibitor - for suppression of TNF-alpha			
PT	and -beta, useful as therapeutic agent.			
PS	Disclosure; Fig 21; 142pp; English.			
CC	The sequence comprises the entire 30 kD TNF inhibitor. The clone			
CC	from which the sequence was deduced was isolated from a cDNA			
CC	library prep. from RNA form U937 cells treated with PMA/PHA.			
CC	The whole gene can be inserted into expression vectors for prepn.			
CC	of TNF inhibitor for use in the treatment of inflammatory and			
CC	degenerative diseases. The active protein is claimed (Claim 8).			
CC	See also R10984 and R11001.			
SQ	Sequence 455 AA;			
Query Match	12.5%;	Score 407;	DB 1;	Length 455;
Best Local Similarity	29.9%;	Pred. No. 5.10e-26;		
Matches 127;	Conservative 81;	Mismatches 177;	Indels 40;	Gaps 32.
Db	27	VIGLVPLHGRKREKRDVSCPOGKYIHPNONSICCTKCKHGYLYNDXCGPGQDTPCRRCES	86	
OY	30	LLGARAGCGTRSPR-CDDA-GDF-HKKIGLFCGCGCPAGHYTKARCTEPCGNSTCLVCPQ	86	
Db	87	GSFPASENHLR-HCLSCSKCKREKGOVEISSCTVDRDTPVCGCRKNQRYRAY-SENLFQC-	143	
OY	87	DTFLAMENHNHNSDCARCOACDEQSAQVALENCSSAVADTRCGCKRGMEVECOVQSSSP	146	
Db	144	FNCSLCIN-GNVH-----LSQENKQNTVC-TCHNGEFLRENDVYSCSNCKKSLSECTKICLP	197	
OY	147	FYCPQCLDCCGLAHNHTRLIC-SRSDTDCGTCLPQFYEHGGGCVSCPSTLIG-SCPERC-A	203	
Db	198	QIENVKGTEDSGTVLPL-LVIFFGCLLSLFLGLMYRYQRMKSLYSIVCKSTPEKE	256	
OY	204	AVCGMRQMF-W-VQVLLAGLVV-PL-LLGATIL-YTTR-HCMPHK-PLVTDAEA-GME	253	
Db	257	GELBCGTTTKPLAPNPSFSPPGFTPTLIGFSVPDSSTFTSSSTYTPGDCPNFAAPREVPAP	316	
OY	254	A-LTPPATNHTSPDSS-AHTL-LAPPDSSSEKICVQLVGNSS-WTPGVPTEQALCPQVT-	308	
Db	317	PYQAGADPLATALLASDPLPNPLCKMDESAIKRPOSLODTPDPAITLYAVENYPLRLKMEFVR	376	
OY	309	-W-SWDQIPSPALSGPALAAPT-LSP-ESPASSPAMMLQPGQ-LYDVADAVPARMKEFVR	363	
Db	377	RLGSLDEHIDRLQNGRCRLREAOYSMLATWRRRTPRRATLLEGLVLRDMGLGCTED	436	
OY	364	TLGLREAIIEAVEVEIGR-FRDQGYEMLKRRRQGP---AGLGAVYALALERMGLDGCVED	419	
Db	437	IEEAL 441		

QY 420 LRSRL 424

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RESULT 14
ID R75084 standard; Protein; 455 AA.
AC R75084;
DE 19-JAN-1996 (first entry)
DE p55 TNF-R.
KM p55: tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KM epidermal growth factor receptor; EGF-R; protease; inhibitor;
KM phorbol myristate acetate; PMA.
OS Homo sapiens.
FH Key
FH peptide Location/Qualifiers
FT /note= "N terminus of soluble p55 TNF-R"
FT modified_site 54..56 "glycosylation site"
FT modified_site 145..147
FT modified_site /note= "glycosylation site"
FT modified_site 161..163
FT /note= "glycosylation site"
FT peptide 193..210
FT /note= "peptide used in creation of chimeras"
FT region 198..210
FT /note= "spacer region"
FT misc_difference 201
FT /note= "major C terminus for soluble p55 TNF-R"
FT misc_difference 202
FT /note= "essential for shedding reaction"
FT misc_difference 203
FT /note= "minor C terminus for soluble p55 TNF-R"
FT region 212..234
FT /note= "transmembrane region"
PN AU9475742-A.
PD 04-MAR-1993.
PD 11-OCT-1994; 075742.
PR 12-OCT-1993; IL-107268.
PA (YEDA ) YEDA RES & DEV CO LTD.
PI Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR MPI: 95-194342/26.
DR N-PSDB: Q90513.
PT New protease capable of cleaving soluble tumour necrosis factor
PT (TNF) receptor - from cell-bound TNF-receptor, useful for
PT antagonising deleterious effects of TNF.
PS Disclosure: Fig 1; 40pp; English.
CC This sequence represents human p55 tumour necrosis factor (TNF-R).
CC Expression of this receptor is regulated by shedding of the extracellular
CC receptor fragment. The p55 TNF-R can be shed in response to different
CC inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC type. The only region of the receptor whose structure affects the
CC shedding response is the spacer region (see R75012) in the extracellular
CC domain. This region is located close to a site of cleavage of the
CC molecule, and links the Cys rich module to the transmembrane domain. The
CC spacer region of the encoded protein was used to create the chimeras
CC between human p55 TNF-R and murine epidermal growth factor receptor
CC (EGF-R) that are represented by R75007-11. This spacer region was
CC subjected to deletion mutations (R75013-25) and substitutions
CC (R75026-47). Of the spacer region, the most important residues are
CC Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC important of these. The shedding of the receptor is independent of the
CC side chain identity of these residues, with the exception of a limited
CC dependence on the identity of Val 173. Mutations which alter the
CC conformation of the protein adversely effect the shedding process.
CC The mutations shown in R75013-47 were introduced in order to create an
CC inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC CC R75017-9, R75025, R75033-5 and R75042-3. These protease inhibitors can
CC be used for enhancing TNF function.
SQ Sequence 455 AA;

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Query Match 12.5%; Score 407; DB 1; Length 455;  
 Best Local Similarity 29.9%; Pred. No. 5,10e-26;  
 Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

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Db 27 VIGLVPHLGDREKRDYSVQPGKYTHPONNSICQTKHKGTYLYNDPCPGQDTPDRCES 86
QY 30 LIGARAGCGTSPR-CODA-GDF-HKKIGLFCRCRCPAGHYLLKACETPCGSGTCLVCPQ 86
Db 87 GSFTASENHLR-HCISCSCKRKGQVEISCTYDRTDYCCGCKKQYHNY-SEMLFQC- 143
QY 87 DTFLAMENHNHNSCARCACCDEQASOVALENCASAVADRCCKPQMFVECOVSQCVSSSP 146
Db 144 FNCISCLN-GTVH----LSCQEKONTVC-TCHAGFLRENECVSCSNCKSLECTKLCIP 197
QY 147 FYCOPCLDCGADHNRHLIC-SRRTDCGTCLPGYEHDGCVSCPSTSLG-SCBERC-A 203
Db 198 QIENYKGTEDSGTIVLP-LVYFFPICLLSLFTGLMRYORWKSILYSYCGKSTPEKE 256
QY 204 AVCGWRQWF-W-VQYLLAGIVV--PL-LLGATLL-YTYR-HCWPKR--PLVYADBA-GME 253
Db 257 GELBGTTKPLAPNPSPTPEFTTLGFSPPSSTFSSSYTTGGDCPNFAPRREAVP 316
QY 254 A-LTPPPATHLSPIDS-AHTL-LAPDSSEKICTVQLVGN-S-WTGGYEPETOALCPQYT- 308
Db 317 PYGADPILATATASDPINPPLQKWECSAHKPOSIDTDDPATLYAVENVPEPLRKFEVR 376
QY 309 -W-SMDQLPSRDLGPAAAPT-LSP-ESPAGSPAMMLQFQPO-LIYMDAVPARMKFEVR 363
Db 377 RUGLSDEHIDRLLEONGRLREAOYSMLATWRRTPRRATLELLGRVLRMDLLGCLLED 436
QY 364 TLGLEAELEAVEVEYIGR-FRDQYEMLRKMRQOP--AGIGAVYAALERMGLGCVBD 419
Db 437 IEEL 441
QY 420 LRSRL 424

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RESULT 15
ID R42059 standard; Protein; 455 AA.
AC R42059;
DE 29-APR-1994 (first entry)
DE Lambda derived TNF-R.
KM Human: tumour necrosis factor receptor; TNF-R; interleukin-1 receptor;
KM IL-1R; fusion protein; linker: TNF; IL-1; cachexia; cerebral malaria;
KM rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;
KM pulmonary fibrosis; silicosis; allograft; xenograft; rejection;
KM graft versus host disease; sepsis; inflammation; allergy;
KM autoimmune dysfunction.
OS Homo sapiens.
OS Lambda-glt10-7ctnfbp.
FH Key Location/Qualifiers
FH peptide 1..40 "Signal peptide"
FT /note= "41..455"
FT protein /note= "Mature hTNF-R"
PN M0931977-A.
PD 14-OCT-1993.
PD 26-MAR-1993; U02938.
PR 30-MAR-1992; US-860710.
PA (IMMV ) IMMUNEX CORP.
PI Smith CA;
DR MPI: 93-336592/42.
DR N-PSDB: Q49932.
PT New fusion protein tumour necrosis factor and human interleukin-1
PT receptor - useful in therapy, diagnosis and assays of e.g.
PT rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.
PS Disclosure: Page 57-59; 85pp; English.
CC The sequences given in R42058-59 represent human tumour necrosis
CC factor receptor (TNF-R) and the sequences in R42060-61 represent
CC human interleukin-1 receptor (IL-1R). These sequences were used in
CC the production of a fusion protein which conformed to one of the
CC formulae:
CC TNF-R-linker-TNF-R-linker-IL-1R
CC IL-1R-linker-TNF-R-linker-TNF-R or
CC TNF-R-linker-TNF-R
The linker may comprise 5-100 amino acids selected from Gly, Asp,

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protein database search, using Smith-Waterman algorithm

Due Jul 25 22:21:31 2000; MasPar time 23.74 Seconds

$\mathcal{C}$  generated.

1 MEETQÖGEAPRGÖLGE\$AA.....ERMGLDGCVEDLRSRLQÖRGP 428

2AM 150

42080 seqs, 47172406 residues

isting first 45 summaries

1:pir1 2:pir2 3:pir3 4:pir4

Mean 47.837; Variance 92.768; scale 0.516

ved by analysis of the total score distribution.

## SUMMARIES

.5	416	1	JN0006	nerve growth factor r	5.03e-07
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45	109	3.3	3707	2	\$18252	heparan sulfate prote	1.13e-01
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## ALIGNMENTS

```
##molecule_type mRNA
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```

##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
REFERENCE
#authors Hummler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
A36555 Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
#journal DNA Cell Biol. (1990) 9:705-715
#title Molecular cloning and expression of human and rat tumor
necrosis factor receptor chain (p60) and its soluble
derivative, tumor necrosis factor-binding protein.
#cross-references MUID:91090841
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
#accession C36555
##molecule_type protein
#residues 30-38:41-53, 'X', 55-79, 'XX', 82-94, 'NK', 'X', 100-104;
107-128:162-167, 'X', 169-201 ##label H12
#title the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor
##note
REFERENCE
#authors A38281
Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
##residues 1-455 ##label GRA
##cross-references GB:M37764
#note The authors translated the codon TGG for residue 371 as
Thr, AAG for residue 372 as Leu, and GAC for residue
427 as Asn
REFERENCE
#authors S12057
Nophr, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang,
R.; Aderka, D.; Holtmann, H.; Wallach, D.
#journal EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-RS).
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:9106021
#accession S12057
##molecule_type mRNA
##residues 1-455 ##label NGP
##cross-references EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing
REFERENCE
#authors JT0758
Kemper, O.; Wallach, D.
#journal Gene (1993) 134:209-216
#title Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#cross-references MUID:94085779
#accession JT0758
##molecule_type DNA
##residues 1-13 ##label KEM
#journal A60231
Seckinger, P.; Vey, E.; Turcatil, G.; Wingfield, P.; Dayer,
J.M.
#journal Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
##residues 41-43, 'X', 45-53, 'X', 55-57 ##label SEC
REFERENCE
A38258

```

```

#authors Gatana, T.; Hwang, C.; Kohn, W.; Cappuccini, E.; Lucci III,
J.A.; Jeffes, E.W.B.; Lantz, R.; Tomlich, J.; Yamamoto,
R.S.; Granger, G.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8781-8784
#title Purification and characterization of an inhibitor (soluble
tumor necrosis factor receptor) for tumor necrosis factor
and lymphotoxin obtained from the serum ultrafiltrates of
human cancer patients.
#cross-references MUID:91062364
#accession A38258
##molecule_type protein
#residues 41-60 ##label GAT
##experimental_source cancer patient serum
REFERENCE
#authors A60594
Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.;
Grubb, A.; Adolf, G.
#journal Eur. J. Haematol. (1989) 42:270-275
#title Isolation and characterization of a tumor necrosis factor
binding protein from urine.
#cross-references MUID:89171156
#accession A60594
##molecule_type protein
#residues 41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 ##label OLS
##experimental_source renal failure patient urine
REFERENCE
#authors A35010
Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession A35010
##molecule_type protein
#residues 41-45 ##label ENG
##experimental_source normal urine
REFERENCE
#authors JC2404
Kajihara, J.; Asada, A.; Kirihaara, S.; Kato, K.
#journal Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title Amino acid sequence of natural tumor necrosis factor alpha
inhibitor purified from human urine.
#cross-references MUID:95128033
#accession JC2404
##molecule_type protein
#residues 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201
##label KAJ
##experimental_source urine
COMMENT This protein is one of two known receptors for both TNF-alpha
(cachectin) and TNF-beta (lymphotoxin).
GENETICS
#gene GDB:TNFR1
#cross-references GDB:125913; OMIM:191190
#map_position 12p13.2-12p13.2
#introns 13/3: 65/71; 108/1; 158/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 1; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-21
22-455
30-211
41-201
44-82
84-126
127-167
168-196
212-234
235-455
54,145,151
SUMMARY
#length 455 #molecular_weight 50494 #checksum 153

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Db	27	VIGLVPHLDREKRDVSCPOGKYIHPQNNNSICCTKCKHKTGYLVNDPCGPDDTCRCRES	86	
QY	30	LGARAGGSTRSR-CDCA-GDF-HKKIGLFCRCRGAGHYLARPCTEPCGNSICLYCPQ	86	
Db	87	GSEFTASENHLR-HCLSCSKCKEMGOVEISSCTVDRTVCGCRKNOYRHYW-SENLFQC-	143	
QY	87	DTFLAMENHNHNSCARCOACDEQASOVALENCASAVADTRCGCKRGWFEQVSQCVSSSP	146	
Db	144	FNCISICLN-GTYV----LSQEKQNTVC-TCHAGFPLRENECVSCNSCKSLSECTKICLP	197	
QY	147	FYCPQPLDGCALRHRLRLIC-SRRDDCGCLTGFEEHGGCVSCPSTIG-SCPERC-A	203	
Db	198	QIENYKGTEDSGTTLVP-LVIFPGCLISLPLIGLRYPRQRMKSRTLYICGSKSTPEKE	256	
QY	204	ANCGMRQM-W-VQVLLAGLV-PL-LIGATITL-TYTR-HCWPHK-PLVTTABEA-GME	253	
Db	257	GELEGTTRKPLAPNPSFPTPGFTPLTGFSPVPSSTFTSSSTYTPGDCPNFAARREVAR	316	
QY	254	A-LTPRPATHLSPIDS-AHTL-LAPDSSBKICTVQVGN-S-WTPGVPEQALCPQVT-	308	
Db	317	PYOGADPIALATALASPIINPFLQKWEBSAKPQSLDTDDPATLYAVENPPLRMKFEVR	376	
QY	309	-W-SWQQLPSRALGPAAPL-LSP-ESPASCPMMLOPGQ-LYDVADAVARRMKFEVR	363	
Db	377	RGLSDHEIDRLONGRCIREAOYSLAWRRRTPREATLELLGVLNDMDLGGTED	436	
QY	364	TIGLRRAELIENAVEYIGR-FRDOQYEMLRKMRQOP---AGLGAVYALERMGIDGVED	419	
Db	437	IEEAL 441		
QY	420	LRSRL 424		
RESULT	2			
ENTRY		GOMST1	#type complete	
TITLE		tumor necrosis factor receptor 1 precursor - mouse		
ALTERNATE_NAMES		tumor necrosis factor receptor, 55k		
ORGANISM		#formal_name Mus musculus; #common_name house mouse		
DATE		30-Jun-1992 #sequence; revision 30-Jun-1992 #text; change 22-Jun-1999		
ACCESSIONS		A38634; B40254; S16677; S19021; I54532		
REFERENCE		A38634		
#authors		Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.		
#journal		Proc. Natl. Acad. Sci. U.S.A. (1991) 88:2830-2834		
#title		Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.		
#cross-references		MUID:91187885		
#accession		A38634		
#molecule_type		mRNA		
#residues		1-454	#label LEW	
#cross-references		GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826		
REFERENCE		A40254		
#authors		Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.T.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.		
#journal		Mol. Cell. Biol. (1991) 11:3020-3026		
#title		Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.		
#cross-references		MUID:91246168		
#accession		B40254		
#molecule_type		mRNA		
#residues		1-454	#label GO2	
#cross-references		GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826		
REFERENCE		S16677		
#authors		Barrett, K.J.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissoneghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.		
#journal		Eur. J. Immunol. (1991) 21:1649-1656		
#title		Cloning, expression and cross-linking analysis of the murine		

```
p53 tumor necrosis factor receptor.
```

```
#cross-references MUID:91285014  
#accession S16677  
##molecule_type mRNA  
##residues 1-454 ##label BAR
```

```
REFERENCE  
#authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
#journal Immunogenetics (1991) 34:338-340  
#title Molecular cloning and expression of the mouse Tnf receptor type b.  
#cross-references EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
```

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REFERENCE  
#accession S19021  
##molecule_type mRNA  
##residues 1-454 ##label ROT
```

```
REFERENCE  
#authors Bebo, B.F.  
#journal Immunogenetics (1994) 39:450-451  
#title Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.  
#cross-references EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
```

```
#accession S15432  
##status translated from GB/EMBL/DDBU  
##molecule_type mRNA  
##residues 1-454 ##label RES
```

```
COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
```

```
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
```

```
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein
```

```
FEATURE  
1-29 domain signal sequence #status predicted #label SIG\  
30-454 #product tumor necrosis factor receptor type 1 #status predicted #label MATV
```

```
30-212 #domain extracellular #status predicted #label EXT\  
4-82 #domain NGF receptor repeat homology #label NG1\  
84-166 #domain NGF receptor repeat homology #label NG2\  
127-167 #domain NGF receptor repeat homology #label NG3\  
168-204 #domain NGF receptor repeat homology #label NG4\  
213-235 #domain transmembrane #status predicted #label MEM\  
236-454 #domain intracellular #status predicted #label INT\  
54,151,202 #binding-site carboxylate (Asn) (covalent) #status predicted
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```
SUMMARY #length 454 #molecular_weight 50129 #checksum 4839
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Query Match 12.2%; Score 399; DB 1; Length 454;  
Best Local Similarity 28.7%; Pred. No. 1,86e+53;  
Matches 119; Conservative 79; Mismatches 182; Indels 34; Gaps 28;
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Dd 40 RDSLCP -GGKVHSHKNNISICTCKHKGYLVSDRPSGRDYVERECKGFTASQNYLR - 97  
| | | | | | | | | | | | | | | | : | : | : | : | : | : | : | : |  
Dd 40 RSPDCDAGD -HKIKGLFCRCRGPAHYIAKAPECTEGCSSTCLVCODDFLAMENHNNS 98  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 98 QLSCKTCRKMSOVETSPCADKDVTGCCKENGFYLTSETHFOCDSCPCNGTWTIP 157  
| | : | : | : | : | : | : | | | | | | | | | | | | | | : |  
Dy 99 ECARQQADDEBSQVALENCASAVADTRCGCKPGFWYC -- QVS -QCYS SSP -FYCQPCLD 154  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 158 CKETD -NTVCNHAGFLRESECVPC - SHCKNEBCKMLCLPPLANTVNPDGSITAYL 214  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Dy 155 CGALHRHTRLLC -SR --- RDTDCGTCLPGFEHGDCGVS -CPTSTLGSC--PERCAAVCG 207  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 215 LPVLIVLLGLCLLSIFISLMCRPYRMRYEVISSICRPVP -VKEEKAKG -ELTPAPSPA F 272  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Dy 208 WKQMWWOYL -LAGIYYVPLL -IGATTL -TYTRYRH -CWPHKKPLVTADEXGMILPPPATIH 263  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```
Dd 273 SPTEGFNFNLTFSTPGFSFPVSP -ISPFI GPSNMHFMPVSEVVYPOTGADPLYESLC 331  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Dy 264 SPLDS -AHTL -LA RPDSSEKI CT YLYGNSTRPYRETGALCPQV -TWMDOLPSRALG 320  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
Dd 332 SVPAETSVQWKEDSAHPDPDNADLATLVAYVDGVPPARKKEFMREMGISEHTERLENO 391  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

OY	321	PAAAPLTISSPSPAS -PAMMLQPC-PQLYDVMDAVPARMKKEVVRITGLREAIIEAVEVE	378
Db	392	NGRCLEKRAQISMLEAMRRRTPRHEDTLEVGYLSKMNLAGCIENTLEAL-RHP	444
OY	379	IGR-FRDOQYEMLRMRQOP--AG-LGAVYAALERMIGDGCVEDLRSLQRP	428
RESULT	3		
ENTRY		JC4302	#type complete
TITLE		tumor necrosis factor receptor p55 precursor - pig	
ORGANISM		formal_name Sus scrofa domestica #common_name domestic pig	
DATE		29-Nov-1995	#status revision 08-Feb-1996 #text_change
ACCESSIONS		JC4302: PC4093	
REFERENCE		JC4302	
authors		Suter, B.; Pauli, U.	
journal		Gene (1995) 163:263-266	
title		Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.	
cross-references		MUID:96011645	
accession		JC4302	
mmolecule_type		mRNA	
residues		1-461	#label SVT
cross-references		GB:U19994; NID:G141752; PIDN:AA048499.1; PID:G1141753	
accession		PC4093	
mmolecule_type		protein	
residues		1-7	#label SV2
experimental_source		kidney cell	line 15
GENETICS			
gene		tnfr	
CLASSIFICATION		#superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology	
KEYWORDS		glycoprotein; kidney; receptor; transmembrane protein; tumor	
FEATURE			
1-29		#domain signal sequence #status predicted #label SIG\	
30-461		#product tumor necrosis factor receptor p55 #status predicted #label MAT\	
44-194		#domain extracellular cysteine rich #status predicted #label EXT\	
44-82		#domain NGF receptor repeat homology #label NG1\	
84-126		#domain NGF receptor repeat homology #label NGF\	
211-231		#domain transmembrane #status predicted #label TM\	
361-447		#domain signal transduction #status predicted #label SIT\	
54,145,151		#binding_site carbohydrate (Asn) (covalent) #status predicted	
SUMMARY		#length 461 #molecular_weight 50696 #checksum 8079	
Query Match		12.2%; Score 398; DB 2; Length 461;	
Best Local Similarity		32.3%; Pred. No. 2,936-53;	
Matches		139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;	
Db	33	HEGDEKRESLCPQKYSHPONRSICCKKHKGYLLHNDCLGPELDDCKEONGTAS	92
OY	36	OGGTSRPR-CDDA-BDF-HKKIGLECCGKAGHILAPCTEPGNSICLVCPDITFLAW	92
Db	93	EHNL-TOCLSCSKCRSEMSOIVEISPCYADPTVCGCRKN--QYR-KY-WSETLF-Q-C	143
OY	93	EHNNHSECKRCQACDEQASOVALENCSAVADPTRCCKRGWVEQVQSCVSSPFYQPC	152
Db	144	LNC-SLCPNGVQLPCLCEKODITCN-CHSGFELRDKECVSCVKNCKMADCKNLCPATSETR	201
OY	153	LDCGALLHRH-T-RLIC-SRRDIDCGTCLPGFHHGDGSCPTSLGSCPERCAAYCGMR	209
Db	202	NDPDTGTIVLLPLVIFPGICLAFLEVGLACRIOR-WKPKLLYSILGCKSPVAVGEDEP	260
OY	210	QMFV--VOVLLA-----GLVPLPLLGATLTYTRHCPHKR-PLV---TA-DEAGMEA	254
Db	261	LMTAPSGGTTTFSPSPSPPTTSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP	320
OY	255	L-TTP-PATILSLPDS-AHTL-LAPDSSSKICTVQVLVNSMTP---GTPFQELALCP	305

Query	Match	Score	DB 2:	Length	454:
321	OGAPILMPAPSPVPTPLPKMGSGSHSA	28.5%	Pred. No. 1.09e-50:		
306	QVTSWMDLP-SRLGLPAAPTL--SPES	79;	Mismatches 183;	Indels 34;	Gaps 28;
381	VRRGLSEHETERIELONGRCLEA				
362	VRTGLRAELEAVEVEIGR-FRQ				
441	EDIEBAL-RGP 450				
418	EDLRSRLQRCGP 428				
RESULT	4				
ENTRY	157826	#type complete			
TITLE	tumor necrosis factor receptor - mouse				
ORGANISM	#formal_name Mus musculus #common_name house mouse				
DATE	02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999				
ACCESSIONS	157826				
REFERENCE	157826				
#authors	Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steilmetz, M.				
#journal	Mol. Immunol. (1993) 30:165-176				
#title	Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.				
#cross-references	MUID:93156721				
#accession	157826	preliminary; translated from GB/EMBL/DBJ			
#status	##molecule_type DNA				
##residues	1-454 ##label RES				
##cross-references	GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102				
GENETICS	TNFR-2				
#gene	13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1				
#intions	#superfamily tumor necrosis factor receptor type 1; NGF				
CLASSIFICATION	receptor repeat homology				
KEYWORDS	cytokine receptor				
FEATURE	#domain NGF receptor repeat homology #label NGF				
44-82	#length 454 #molecular_weight 50030 #checksum 4267				
SUMMARY					
Query	Match	Score	DB 2:	Length	454:
Best Local Similarity	28.5%;	Pred. No. 1.09e-50:			
Matches	118; Conservative	79;	Mismatches 183;	Indels 34;	Gaps 28;
40	RDSLCP-OGKYVHKNKNSICTKHKGT				
40	RSPRODAGDF-HKRTGLFCRCGPAGHY				
98	QCLSCCTCKEKESQYEISPCQADKDT				
99	ECARQACDEQASQVALENCASVAADT				
158	CKETO-NWYCNCHAFPLRESRCVPC--				
155	CGALHHRHRLD-SR--RDIDCGTCL				
215	LPLVILIGLCLSPITFISIMCYRPMR				
208	WQOMFVWQV-LLAGLVPLL-LGATL				
273	SPTSGFNPLGFTSGFSSVSSIP-ISP				
264	SPIDS-AHTL-LAPDSSEKICTVQ				
332	SVPAPIVSQKMDSAHPQRPNDADAL				
321	PAAPPLSPESPAGS-PAAMIQPG-P				
392	NGGCLREAYSMLEAMRRTPRHEDT				
379	TGR-FDQDYELMKRRQGP--AG-L				

ENTRY	5	RESULT
TITLE	GOR11	#type complete
CONTAINS	tumor necrosis factor receptor 1 precursor - rat	
ORGANISM	tumor necrosis factor binding protein 1 (TNF blocking factor)	
DATE	#formal_name Rattus norvegicus #common_name Norway rat	
	30-Jun-1992	#sequence_revision 07-Oct-1994
	22-Jun-1999	#text_change
ACCESSIONS	B36555	
AUTHORS	Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizmaier, K.; Lantzi, M.; Olsson, I.; Hauptmann, R.; Stratawa, C.; Adolf, G.R.	
#journal	DNA Cell Biol. (1990) 9:705-715	
#title	Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein.	
#cross-references	MUID:91090841	
#accession	B36555	
#molecule_type	mRNA	
#residues	1-461	#label HIM
#cross-references	GB:M63122; NID:g207361; PIDN:AAA42556.1; PID:g207362	
COMMENT	This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).	
CLASSIFICATION	#superfamily tumor necrosis factor receptor type 1; NCF receptor repeat homology	
KEYWORDS	duplication; glycoprotein; receptor; transmembrane protein	
FEATURE		
1-29	#domain signal sequence #status predicted #label SIG	
30-461	#product tumor necrosis factor receptor type 1 #status predicted #label MAT	
30-211	#domain extracellular #status predicted #label EXT	
30-201	#product tumor necrosis factor binding protein #status predicted #label TBP	
44-82	#domain NCF receptor repeat homology #label NG1	
84-166	#domain NCF receptor repeat homology #label NG2	
127-167	#domain NCF receptor repeat homology #label NG3	
168-204	#domain NCF receptor repeat homology #label NG4	
212-234	#domain transmembrane #status predicted #label MEM	
235-461	#domain intracellular #status predicted #label INT	
54,151,201	#binding_site carbohydrate (Asn) (covalent) #status predicted	
SUMMARY	#length 461 #molecular_weight 50969 #checksum 1617	
Query Match	11.7%; Score 383; DB 1; Length 461;	
Best Local Similarity	29.8%; Pred. No. 2,72e-50;	
Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;		
Db	35 GDBREKRDNLCPGKGAHPNNSICGCKHKTGLVSDPCSPGQETVCEVDKGTFTASON 94	
QY	38 GTRSRCPD-CA-GDF-HKKTIGLFCGCGAGHATKAPCTEPCGNSCTVLPQDTFLAMEN 94	
Db	95 H-VROCLSGKTCRKEHFOVEISPCKADMDTVCGCKRNGFORLYSETHFGQVDCSPCENG 153	
QY	95 HNSSECARCOADEQASQVALENCASVAADTCGCKGWEFEC--QVS-QCVSSSP-FYCO 150	
Db	154 VTPEKE-KONTVNCNCHAGFLISGNCPTCSHCKKNOEGCKKLLPVPANTNTNODSTAV 212	
QY	151 PCLDGLAHRRRLICSRDTCGT-CLP-GLEYHGDGVS-C-PTSTLASCPCERCAVC 206	
Db	213 LLPLVIFGLCLPFLICISLRCRYPQWRPRVYSIICRDSAPVKEVEGEGIVTPPLTPASI 272	
QY	207 GWRQFWYQV--LLAGLVPLL--LGATLVYTRH-CMPKPLVLTADAGM--EATLPPA 260	
Db	273 PAFSGNPGFNPLGISTTPRFSHPVSTPISPVEGFSNMHNFPVRYEVPTQ-G-A-DP 329	
QY	261 THLSPLDS-AHTL-LAP-PDSSEKICTVOL-V-GMS-WTPGYPEQEAALCPQVTSMDQ 313	
Db	330 LLYGSLNVPPIPAVPRKMDVVAAPORLDTDPALVLVVDVDPTRKMEFRRLGLSE 389	
QY	314 LPSRALGAAAPVT-LSP-ESPAQSPAMMLQPG-PQ-LTYMDMDVPAARRKKEFVPTGLRE 369	

Db	390	HEERLELNGRCLEBRAHNSMLARRRRPRRHEATLIDVGRVCLDMLRGCLREIRETLE	449
OY	370	AETAEAVEVEIGR-FRDOQTEMLKRWROOP--AGLGAVYAALERMGLDGVEDLRSRLQ	425
RESULT	6	JC2395	#type complete
ENTRY		Fas antigen precursor - rat	
TITLE		#formal_name Rattus norvegicus #common_name Norway rat	
ORGANISM		20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change	
DATE		16-Jul-1999	
ACCESSIONS		JC2395: PC2246	
REFERENCE		JC2395	
#authors		Kimura, K.; Wakatsuki, T.; Yamamoto, M.	
#journal		Biochem. Biophys. Res. Commun. (1994) 198:666-674	
#title		A variant mRNA species encoding a truncated form of Fas antigen in the rat liver.	
#cross-references		MUID:94128114	
#accession		JC2395	
#molecule_type		mRNA	
#residues		1-324	#label KIM
#cross-references		DDBJ:D26113; NID:9468486; PID:d1005650; PID:g468487	
#experimental_source		thymus	
#accession		PC2246	
#molecule_type		mRNA	
#residues		1-62, 'RPT', #label KIT	
#cross-references		DDBJ:D26113; NID:9468488; PID:d1005651; PID:g468489	
#experimental_source		liver	
GENETICS			
#introns		62/1	
CLASSIFICATION		superfamily NCF receptor repeat homology	
KEYWORDS		transmembrane protein	
FEATURE			
1-21		#domain signal sequence #status predicted #label SIG\	
22-324		#product Fas antigen #status predicted #label MAT\	
44-79		#domain NCF receptor repeat homology #label NCF\	
81-124		#domain NCF receptor repeat homology #label NG4\	
111-188		#domain transmembrane #status predicted #label TMM	
SUMMARY		#length 324 #molecular_weight 36835 #checksum 7305	
Query Match		6.5%: Score 211; DB 2: Length 324:	
Best local Similarity		30.1%: Pred. NO. 7.50e-18;	
Matches		37; Conservative 26; Mismatches 47; Indels 13; Gaps 12;	
Db	43	NCSEGLYQ-VGPEFCPCPCGGERKVD-CTTSGAPTCHPCTGEEYTDK-KHYSDCR 99	
OY	45	DCAGDPHKIKIGLFCGCGCAG-HYLKAPCTPCGNGSTCLVCPQ-DPTLAENHNHNSPCAR 102	
Db	100	CAFCDGHCLEVE-TNCTRTQNTKCKKENFY--CNASLC-DHC-YHCTSCGLE-DILEP 153	
OY	103	COACDE-QASQVALENCASVADTRCCKPGMFVECVQVSCVSSSPFYCPC-LDCGALHR 160	
Db	154	CMR 156	
OY	161	HTR 163	
RESULT	7	A46484	#type complete
ENTRY		apoptosis-mediating membrane-associated polypeptide Fas - mouse	
TITLE		#formal_name Mus musculus #common_name house mouse	
ORGANISM		18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change	
DATE		16-Jul-1999	
ACCESSIONS		A46484; A47254	
REFERENCE		A46484	
#authors		Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;	
#journal		Copeland, N.G.; Jenkins, N.A.; Nagata, S.	
#title		J. Immunol. (1992) 148:1274-1279	
#cross-references		The cDNA structure, expression, and chromosomal assignment of the mouse Fas antigen.	
#accession		A46484	

```

#status      preliminary
##molecule_type mRNA
##residues   1-327 ##label MAT
##cross-references GB:M83649; NID:g193225; PID:g193226
##experimental_source BAM3 macrophage cell line
##note       sequence extracted from NCBI backbone (NCBIN:81544,
              NCBI:P81545)

REFERENCE
#authors     A47254
#journal      Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
#title        Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
              aberrant transcription caused by the insertion of an early
              transposable element in an intron of the Fas antigen gene
              of lpr mice.
#cross-references MUID:93189576
#accession   A47254
##status     preliminary
##molecule_type nucleic acid
##residues   1-96 ##label ADA
##cross-references GB:S56490; NID:g298505; PID:g298506
##experimental_source MRI, lpr/lpr
##note       sequence extracted from NCBI backbone (NCBIN:126850,
              NCBIN:126853, NCBIN:126863, NCBI:P126864)

CLASSIFICATION
KEYWORDS     #superfamily NGF receptor repeat homology
FEATURES     transmembrane protein
44-79
81-124
SUMMARY      #domain NGF receptor repeat homology #label NGF\
              #domain NGF receptor repeat homology #label NG4
              #length 327 #molecular-weight 37417 #checksum 8479

Query Match          6.2%; Score 204; DB 2; Length 327;
Best Local Similarity 27.9%; Pred. No. 1.26e-16;
Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;

Db    43 NCSEGIYOG-GPFCPCOPCPGKKKRVDDCKMNGSTPTCAPCTEKEYYD-KNHVADKCRCR 100
      :|:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Oy    45 DQAGDFHKKIGLFGCGCGCPRAGHYLKAPCTEPCCNSICLVGPDPDT-FLAMENHHNSECARC 103
      ||:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Db    101 TLCDDEHGLEVEFTNCTLTONTKCKCRPDYDCSPGCHECYRAS 144
      ||:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Oy    104 QACDEQASQVALENCSAVDTRCGCKRPGEWEICOVS-QCVSSPS 146

RESULT      8
ENTRY       137383 #type complete
TITLE       FAS soluble protein - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
            02-Jul-1996
ACCESSIONS  137383
REFERENCE   137383
#authors     Gasclino, I.; Finucci, G.; Papoff, G.; Ruberti, G.
#journal      J. Immunol. (1995) 154:2706-2713
#title        Three functional soluble forms of the human
              apoptosis-inducing Fas molecule are produced by alternative
              splicing.
#cross-references MUID:95181785
#accession   137383
##status     preliminary; translated from GB/EMBL/DDBJ
##molecule_type mRNA
##residues   1-314 ##label RES
##cross-references EMBL:Z47993; NID:g728578; PID:g695539
SUMMARY      #length 314 #molecular-weight 35386 #checksum 655

Query Match          5.88; Score 190; DB 2; Length 314;
Best Local Similarity 34.1%; Pred. No. 3.26e-14;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

Db    56 GOFCHRPCCPGE-RKRARDGVNGDEDPCCVCQEQEKETTD-KAHSSSKRCRRLCDGHGL 113
      |:::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Oy    55 GLFCCGCGCPRAGHYLKAP-CTEPCCGNSICLVGPDPDT-FLAMENHHNSECARCQACDF-QAS 111
      ::||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

Db    114 EVEI-NCTRPTONTCKRCRKPFFCNSTVCEHC 143
      ::||::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

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QY      112 QVAFENCASVADTRCGCKRGMFVECOVVS-QC 141
RESULT  9
ENTRY   A40036 #type complete
TITLE   apoptosis-mediating surface antigen Fas precursor - human
ALTERNATE_NAMES
ORGANISM #formal_name Homo sapiens #common_name man
DATE     17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
10-Sep-1997

ACCESSIONS
REFERENCE A40036; S24543; A38142
#authors Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima,
S.I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.
#journal Cell (1991) 66:233-243
#title The polypeptide encoded by the cDNA for human cell surface
antigen Fas can mediate apoptosis.
#cross-references MUID:91309137
#accession A40036
#status preliminary
#molecule_type mRNA
#residues 1-335 #label ITO
#cross-references GB:M67454; NID:g182409; PID:g182410
S24543

REFERENCE
#authors Krammer, P.H.
#submission submitted to the EMBL Data Library, February 1992
#accession S24543
#status preliminary
#molecule_type mRNA
#residues 1-335 #label KRA
#cross-references EMBL:X63717; NID:g28741; PID:g28742
A38142

REFERENCE
#authors Gehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Mater, G.;
Klas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trautsh,
B.C.; Conning, H.; Krammer, P.H.
J. Biol. Chem. (1992) 267:10709-10715
#journal Purification and molecular cloning of the APO-1 cell surface
antigen, a member of the tumor necrosis factor/nerve growth
factor receptor superfamily. Sequence identity with the Fas
antigen.
#title

#cross-references MUID:92268122
#accession A38142
#status preliminary: not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-134, 'Q', 136-335 #label OEH
#experimental_source SKW6.4 cells
#note sequence extracted from NCBI backbone (NCBIP:103810)
#note in NCBI backbone the source is designated as mouse
GENETICS
#gene GDB:APT1
#cross-references GDB:132671; OMTM:134637
#map_position 10q24.1-10q24.1
CLASSIFICATION
KEYWORDS #superfamily NCF receptor repeat homology
apoptosis; surface antigen; transmembrane protein
FEATURE
1-16 #domain signal sequence #status predicted #label SIG\
15-128 #domain NCF receptor repeat homology #label NG4\
174-190 #domain transmembrane #status predicted #label TMM
SUMMARY #length 335 #molecular_weight 37732 #checksum 4899

Query Match 5.8%; Score 190; DB 2; Length 335;
Best local Similarity 34.1%; Pred. No. 3,26e-14;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

DB      56 GOFCHKPCPPGF-RKARDCITGVGDEPDVCFQDSKETTD-KAIFSSKCRKRCRLCDEBGL 113
111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 :
QY      55 GFCCGCGCPAGHLYKAP-CTEPGCGNSTCIWCPDT-FLAMENHNHNSCARCQACDE-QAS 111
111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 :
DB      114 EVEI-NCTRTQNTCKCKRPFNFCNSTYCEHC 143
111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 : 111 :
QY      112 QVAFENCASVADTRCGCKRGMFVECOVVS-QC 141

```

ENTRY	10	QGVZML	#type complete
TITLE		T2 protein - myxoma virus (strain Lausanne)	
ORGANISM		#formal_name myxoma virus	
DATE		31-Dec-1992	#text_change 31-Dec-1992
ACCESSIONS		A40566	
REFERENCE		A40566	
#authors		Upton, C.; Maceu, J.L.; Schreiber, M.; Mcfadden, G.	
#journal		Virology (1991) 184:370-382	
#title		Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor receptor gene family that contributes to viral virulence.	
#cross-references		MUID:91335768	
#accession		A40566	
#molecule_type		DNA	
#residues		1-326	#label UPT
#cross-references		GB:M95181; GB:M7976; NID:g332309; PIDN:AAA46632.1; PID:g9332210	
CLASSIFICATION		#superfamily myxoma virus T2 protein; NGF receptor repeat homology	
KEYWORDS		glycoprotein	
FEATURE			
64-105		#domain NGF receptor repeat homology	#label NG2\
106-147		#domain NGF receptor repeat homology	#label NG3\
66,181,205,238		#binding_site carbohydrate (Asn) (covalent)	#status predicted
SUMMARY		#length 326	#molecular_weight 35208 #checksum 9255
Query Match		5.6%;	Score 182; DB 1; Length 326;
Best Local Similarity		30.9%;	Pred. No. 7,40e-13;
Matches		34;	Conservative 23; Mismatches 45; Indels 8; Gaps 8;
Db		5	TLLIAYVACVGGAGPYGADRGKRGNDYKDL-CTSCPPGYSARLCG-PCSDPVS 62
		25	ALLLVILGARGQGT-R-SP-RCDAGPFHKIGLFCRCRGCPAGHYLKAPTEPCGNSTCL 82
Db		63	PKKNETTTA-STNHAAPACVSCRGHCTGLSE-S-QSCDKTRDRYCDSCAG 109
QY		83	VCPODTFLAMENHHNSECARCOA-CDBOASQVALENCSSAVALDFRCGCKP 131
RESULT	11		
ENTRY		D36858	#type complete
TITLE		gene G4R protein - variola virus	
ALTERNATE_NAMES		B28R protein (COP)	
ORGANISM		#formal_name variola virus	
DATE		30-Sep-1993	#sequence_revision 30-Sep-1993
ACCESSIONS		A36859	
REFERENCE		D36858; S46888; S32385; S35987	
#authors		Blinov, V.M.	
#submission		submitted to Genbank, November 1992	
#description		not shown.	
#accession		D36858	
#status		Preliminary	
#molecule_type		DNA	
#residues		1-349	#label BLI
#cross-references		GB:X69198; NID:g456758; PID:g457087	
#experimental_source		strain India-1967, ssp. major, isolate Ind3	
REFERENCE		S46868	
#authors		Kolykhalov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, I.V.; Totmenin, A.V.; Shchelkunov, S.N.; Sandakhtchey, L.S.	
#submission		submitted to the EMBL data library, April 1992	
#description		Nucleotide sequence analysis of the region of variola virus XhoI F O H P Q genome fragment.	
#accession		S46888	
#status		Preliminary	
#molecule_type		DNA	
#residues		1-349	#label KOL
#cross-references		EMBL:X67117; NID:g516428; PID:g516449	
#experimental_source		strain India-1967, isolate Ind3	

```

REFERENCE      S32385
#authors      Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
#journal      FEBS Lett. (1993) 319:80-83
#title        Genes of variola and vaccinia viruses necessary to overcome
               the host protective mechanisms.
#cross-references MUID:93202281
#accession    S32385
#molecule_type DNA
#residues     31-168 ##label SHC
#cross-references EMBL:X69198
#experimental_source strain India-1967, ssp. major

GENETICS
#gene         G4R
               #superfamily myxoma virus T2 protein; NGF receptor repeat
               homology

FEATURE
33-66         #domain NGF receptor repeat homology #label NGF\
68-109        #domain NGF receptor repeat homology #label NG2\
110-151       #domain NGF receptor repeat homology #label NG3\

SUMMARY
               #length 349 #molecular-weight 38189 #checksum 2016

Query Match      5.5%; Score 179; DB 2; Length 349;
Best Local Similarity 27.1%; Pred. NO. 2,36e-12;
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7

Db      15 IINCRDAFTTPPGKKKDTLEY-KRHH-CCLSCPFTYASRLC-DSKTTQCTPCGSG 71
QY      29 VLLGARAGGGRSPKCD-AGDFHKIKILFFCRRCPAGHYLAKAPCTEPCGNSSTLCPPQD 87

Db      72 TTTSTNNHL-PACLSGNGRCN-SNOVETRSCTNTHHNICCSGPY 115
QY      88 TFLAENHNHSECARCQA-CDEQASQVALAEMCSAVALDRCGCKRGWF 133

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RESULT      12
ENTRY
TITLE      A46517      #type complete
ALTERNATE_NAMES      CD27 antigen precursor - human
ORGANISM      CD27L receptor; T cell activation antigen CD27
DATE      #format_name Homo sapiens #common_name man
          18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change
          22-Jun-1999
ACCESSIONS      A46517; A46454
REFERENCE
#authors      Loeenen, W.A.; Gravelstein, L.A.; Beumer, S.; Meljief, C.J.;
          Hagemeijer, A.; Borst, J.
#journal      J. Immunol. (1992) 149:3937-3943
#title      Genomic organization and chromosomal localization of the
          human CD27 gene.
#cross-references MIMD:93094588
#accession      A46517
#status      not compared with conceptual translation
#molecule_type DNA
##residues      1-260 ##label LOE
#note      sequence extracted from NCBI backbone (NCBIP:120386)
          authors propose an alternative repeat pattern
REFERENCE      A46454
#authors      Cammerlind, D.; Walz, G.; Loeenen, W.A.; Borst, J.; Seed, B.
#journal      J. Immunol. (1991) 147:3165-3169
#title      The T cell activation antigen CD27 is a member of the nerve
          growth factor/tumor necrosis factor receptor gene family.
#cross-references MIMD:92013149
#accession      A46454
#molecule_type mRNA
##residues      1-58, 'A', 60-260 ##label CAM
#cross-references GB:M63928; MIMD:g180084; P1DN:AA58411.1; P1D:g180085
#note      sequence extracted from NCBI backbone (NCBIN:60285,
          NCBIP:60289)
COMMENT      A soluble CD27 found in serum and urine is formed by proteolysis.
GENETICS
#gene      GDB:CD27
##cross-references GDB:132582; OMIM:186711
#map_position 12p13-12p13
#introns      467/1: 90/5; 150/4: 180/1; 220/1

```







```

#journal      J.L.
#title        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8331-8335
#cross-references MUID:91045991
#accession    A36475
#status       preliminary
#molecule_type mRNA
#residues     1-195,'R',197-461 ##label KOH
#cross-references GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1;
                PID:9339758
REFERENCE
#authors      Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.;
#journal      Gentz, R.; Brockhaus, M.; Lesslauer, W.
#title        Cytokine (1990) 2:231-237
#cross-references MUID:91370690
#accession    A48416
#status       preliminary
#molecule_type mRNA; protein
#residues     23-461 ##label DBM
#cross-references GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
#note         sequence extracted from NCBI backbone (NCBIN:63368,
                NCBI:P:63371)
REFERENCE
#authors      Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang,
#journal      D.; Ringold, G.M.
#title        Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
#cross-references MUID:90349572
#accession    A36007
#status       preliminary
#molecule_type mRNA
#residues     116-140,'P',142-195,'R',197-362,'T',364-461 ##label HBL
#cross-references GB:M5857; NID:9339751; PIDN:AAA63262.1; PID:9339752
REFERENCE
#authors      Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.;
#journal      Lesslauer, W.; Brockhaus, M.
#title        J. Biol. Chem. (1990) 265:20131-20138
#cross-references MUID:91056448
#accession    A23666
#status       preliminary
#molecule_type protein
#residues     23-40;65-69;136-141;300-306 ##label LOE
REFERENCE
#authors      Engelmann, H.; Novick, D.; Wallach, D.
#journal      J. Biol. Chem. (1990) 265:1531-1536
#title        Two tumor necrosis factor-binding proteins purified from
                human urine. Evidence for immunological cross-reactivity
                with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession    B35010
#status       preliminary
#molecule_type protein
#residues     27-31 ##label ENG
REFERENCE
#authors      Kuhnert, P.; Kemper, O.; Wallach, D.
#journal      Gene (1994) 150:381-386
#title        Cloning, sequencing and partial functional characterization
                of the 5' region of the human p75 tumor necrosis factor
                receptor-encoding gene (TNF-R).
#cross-references MUID:95121934
#accession    I38094
#status       preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues     1-37 ##label RES
#cross-references EMBL:X80021; NID:9666044; PIDN:CAA56324.1;
                PID:9825701
GENETICS

```

```

#gene          GDB:TNFR2
##cross-references GDB:125914; OMIM:191191
#map_position  1p36.2-1p36.2
#introns       26/3
#note          the list of introns is incomplete
CLASSIFICATION #superfamily tumor necrosis factor receptor type 2; NGF
                receptor repeat homology
                duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-22          #domain signal sequence #status predicted #label Sig\
23-416        #product tumor necrosis factor receptor type 2 #status
                experimental #label MAT\
40-76         #domain NGF receptor repeat homology #label NG1\
78-119        #domain NGF receptor repeat homology #label NG2\
120-162       #domain NGF receptor repeat homology #label NG3\
164-201       #domain NGF receptor repeat homology #label NG4\
262-279       #domain transmembrane #status predicted #label TMN\
280-461       #domain intracellular #status predicted #label INT\
171,193       #binding site carbohydrate (Asn) (covalent) #status
                predicted
SUMMARY
#length 461 #molecular-weight 48291 #checksum 5724
Query Match      5.1%; Score 168; DB 1; Length 461;
Best local Similarity 27.6%; Pred. No. 1.56e-10;
Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;
Db      44 EYDQTAQMCCKSCSPQAHAKVFCTKT-SPTVCDSCEDSTYTQIW-NW-VPECLSCGSRG 100
      49 DFHKKIGLFCCRCRCPAGHYLAKPCTEPCGNSGLVCPQDFLA-WENHNNSECARCOA-C 106
      101 S--SDQYETQACTREQNRICTCRPGWY 125
      107 DEQASQVALENCSAVADTRCGCKRPGWF 133
Search completed: Tue Jul 25 22:21:58 2000
Job time : 27 secs.

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WIDEOR (TM)

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Msrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jul 25 22:20:36 2000; Maspar time 36.30 Seconds

Tabular output not generated. 817.386 Million cell updates/sec

Title: >US-09-314-889-2  
Description: (1-428) from US09314889.pep  
Perfect Score: 3267  
Sequence: 1 MEETQGEARQGLRGESAA.....ERMGLDQVEDLRSLQGRP 428

Scoring table: PAM 150  
Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: spltembl12  
1:sp.archaea 2:sp.bacteria 3:sp.fungi 4:sp.human  
5:sp.invertebrate 6:sp.mammal 7:sp\_mmc 8:sp.organella  
9:sp.phage 10:sp\_plant 11:sp\_todent 12:sp\_unclassified  
13:sp\_vertebrate 14:sp\_virus

Statistics: Mean 47.496; Variance 85.662; scale 0.554

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3107	95.1	418	4	000275	LYMPHOCYTE ASSOCIATED	0.00e+00
2	2865	87.7	426	4	014865	DEATH RECEPTOR 3 BETA.	0.00e+00
3	2451	75.0	372	4	000279	LYMPHOCYTE ASSOCIATED	0.00e+00
4	2403	73.6	380	4	000280	LYMPHOCYTE ASSOCIATED	0.00e+00
5	1497	45.8	253	4	000276	LYMPHOCYTE ASSOCIATED	0.00e+00
6	1343	41.1	277	4	014866	SOLUBLE DEATH RECEPTOR	1.19e-271
7	1329	40.7	234	4	000278	LYMPHOCYTE ASSOCIATED	2.14e-268
8	467	14.3	126	4	000277	LYMPHOCYTE ASSOCIATED	2.63e-72
9	272	8.3	471	6	019131	TUMOR NECROSIS FACTOR-	2.91e-31
10	218	6.7	327	6	097491	FAS PROTEIN.	1.13e-20
11	213	6.5	616	4	097606	RECEPTOR ACTIVATOR OF	1.01e-19
12	210	6.4	189	6	097530	TUMOR NECROSIS FACTOR	3.74e-19
13	206	6.3	189	6	095185	TUMOR NECROSIS FACTOR	2.12e-18
14	202	6.2	263	6	09X820	FAS ANTIGEN SPLICED VA	1.19e-17
15	202	6.2	320	6	09X829	C-TYPE FAS ANTIGEN.	1.19e-17
16	202	6.2	625	11	035305	RECEPTOR ACTIVATOR OF	1.19e-17
17	199	6.1	186	14	072735	A53R PROTEIN.	4.33e-17
18	198	6.1	186	14	097P87	SOLUBLE TNF RECEPTOR C	6.64e-17
19	200	6.1	316	14	057092	TUMOR NECROSIS FACTOR	2.82e-17
20	194	5.9	186	14	09WJ84	TUMOR NECROSIS FACTOR	3.66e-16

21	193	5.9	283	4	092956	HERPESVIRUS ENTRY MEDI	5.60e-16
22	190	5.8	283	6	09XS28	HEVANS.	2.00e-15
23	190	5.8	314	4	014293	FAS SOLUBLE PROTEIN.	2.00e-15
24	188	5.8	320	14	057300	TUMOR NECROSIS FACTOR	4.64e-15
25	188	5.8	320	14	057091	TUMOR NECROSIS FACTOR	7.07e-15
26	187	5.7	322	14	072761	K2R PROTEIN.	1.32e-13
27	180	5.5	349	14	057109	TUMOR NECROSIS FACTOR	2.00e-13
28	179	5.5	349	14	089118	SOMALIA-1977 RIGHT NEA	2.00e-13
29	179	5.5	349	14	057111	TUMOR NECROSIS FACTOR	2.00e-13
30	179	5.5	349	14	057110	TUMOR NECROSIS FACTOR	2.00e-13
31	179	5.5	349	14	089098	GARCIA-1966 RIGHT NEAR	2.00e-13
32	178	5.4	348	14	057112	TUMOR NECROSIS FACTOR	3.03e-13
33	178	5.4	348	14	085407	HOMOLOG OF VACCINIA VI	3.03e-13
34	175	5.4	350	14	057116	TUMOR NECROSIS FACTOR	1.04e-12
35	174	5.3	348	14	057103	TUMOR NECROSIS FACTOR	1.58e-12
36	174	5.3	348	14	057108	TUMOR NECROSIS FACTOR	1.58e-12
37	174	5.3	348	14	057277	TUMOR NECROSIS FACTOR	1.58e-12
38	174	5.3	349	14	057098	TUMOR NECROSIS FACTOR	1.58e-12
39	174	5.3	349	14	057099	TUMOR NECROSIS FACTOR	1.58e-12
40	174	5.3	349	14	057291	TUMOR NECROSIS FACTOR	1.58e-12
41	174	5.3	349	14	057102	TUMOR NECROSIS FACTOR	1.58e-12
42	174	5.3	349	14	057101	TUMOR NECROSIS FACTOR	1.58e-12
43	174	5.3	349	14	057100	TUMOR NECROSIS FACTOR	1.58e-12
44	174	5.3	349	14	057284	TUMOR NECROSIS FACTOR	1.58e-12
45	174	5.3	355	14	085308	SECRETED RECEPTOR BIND	1.58e-12

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	418 AA.
AC	000275			
DT	01-JUL-1997 (TREMUREL. 04, Created)			
DT	01-JUL-1997 (TREMUREL. 04, Last sequence update)			
DT	01-NOV-1999 (TREMUREL. 12, Last annotation update)			
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 1B.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97272273.			
RA	SCREATION G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,			
RA	MCMICHAEL A.J., BELL J.I.,			
RT	"LARD: a new lymphoid-specific death domain containing receptor			
RT	RT, sequenced by alternative pre-mRNA splicing."			
RI	Proc. Natl. Acad. Sci. U.S.A. 94:1615-1619(1997).			
DR	EMBL: U94502; AAC51307.1; -			
DR	HSSP: P19438; 1TNR			
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.			
DR	PFAM: PF00531; death; 1.			
DR	PFAM: PF00020; TNFR_c6; 2.			
SQ	SEQUENCE 418 AA; 45456 MW; 3D04954A CRC32;			
Query Match	Score 3107; DB 4; Length 418;			
Best Local Similarity	98.1%; Pred. No. 0.00e+00;			
Matches	407; Conservative 3; Mismatches 4; Indels 1; Gaps 1;			
Db	4 RPRCAVAAALLLVLLGARAGGTRSPRCDAGDFHKITGLFCRCRGPAGHYLKAPCTE 63			
Qy	15 RGEAAVPPQALLLVLLGARAGGTRSPRCDAGDFHKITGLFCRCRGPAGHYLKAPCTE 74			
Db	64 PCGNSTLVCPDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 123			
Qy	75 PCGNSTLVCPDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRCGCKPGMFV 134			
Db	124 ECVQSVQVSSPFCQPCDCLGALHRTTRILCSRRDDCGCLGFEHGGCVSCPST 183			
Qy	135 ECVQSVQVSSPFCQPCDCLGALHRTTRILCSRRDDCGCLGFEHGGCVSCPST 194			
Db	184 LGSCEPACAVCGRMQFNVQVLLAGLVPLLLGATLTYTYRHCMKPKPLTAADEAGME 243			
Qy	195 LGSCEPACAVCGRMQFNVQVLLAGLVPLLLGATLTYTYRHCMKPKPLTAADEAGME 253			

OY	426 RGP 428
II	
RESULT	3
ID	000279
AC	000279;
DT	01-JUL-1997 (TREMblrel. 04, Created)
DT	01-JUL-1997 (TREMblrel. 04, Last sequence update)
DT	01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE	LYMPHOCTE ASSOCIATED RECEPTOR OF DEATH 8
DE	(LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 5).
OS	Homo sapiens (Human)..
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Xenarthra; Primates; Catarrhini; Homnidae; Homo.
RN	[1]
RP	SEQUENCE FROM N.A..
RA	SCEARON G., XU X.N., OLSEN A., COMPER A., TAN R., MCMICHAEL A.,
RA	BELL J.;
RL	Submitted (MAY-1997) to the EMBL/GenBank/DDBU databases.
DR	EMBL; U94509; AAC51314.1; -
DR	EMBL; U94506; AAC51311.1; -
DR	HSSP; P19438; IYR.
DR	PFAW; PF00531; death; 1.
KW	Alternative splicing
SO	SEQUENCE 372 AA; 40391 MW; 430DA0D5 CRC32;

Query Match	75.0%	Score 2451	DB 4	Length 372
Best Local Similarity 98.5%	Pred. No. 0.00e+00	Mismatches 2	Indels 1	Gaps 1
Matches 321	Conservative	2		
Db	48	CRGCPA-ASQVALENCASVADTRCGCKRGMFVEVCQVSSSPFYCPCLDGCALHRT	106	
Oy	103	COACDEASQVVALENCASVADTRCGCKRGMFVEVCQVSSSPFYCPCLDGCALHRT	162	
Db	107	RLICRRPTDGCGLPGHYEHGDCVCSPTSLSCPCRCAAVCGMFMVQVLLAGLV	166	
Oy	163	RLICRRPTDGCGLPGHYEHGDCVCSPTSLSCPCRCAAVCGMFMVQVLLAGLV	222	
Db	167	VLILGATLTYTYRHCWPHKPLVTADEAGMALTPPAATHLSPLDSATHLLAPDSSEKI	226	
Oy	223	VLILGATLTYTYRHCWPHKPLVTADEAGMALTPPAATHLSPLDSATHLLAPDSSEKI	282	
Db	227	CTVOLVGNSSWTPRGPRETOEALCPQVYWSMDLPFSAALCPAAPTLPSPSPAGSAMMLQP	286	
Oy	283	CTVOLVGNSSWTPRGPRETOEALCPQVYWSMDLPFSAALCPAAPTLPSPSPAGSAMMLQP	342	
Db	287	GGQILDVMDVADPARRKKEFVRTLIGLREAEIEAVEIGREFPDQOYEMLKRKROOPAGLG	346	
Oy	343	GGQILDVMDVADPARRKKEFVRTLIGLREAEIEAVEIGREFPDQOYEMLKRKROOPAGLG	402	
Db	347	AVYAALERMGIDGCEDELSRLONGP	372	
Oy	403	AVYAALERMGIDGCEDELSRLONGP	428	
RESULT	4	PRELIMINARY:	PRT:	380 AA.
ID	000280			
AC	000280			
DT	01-JUL-1997	(TREMBlrel. 04, Created)		
DT	01-JUL-1997	(TREMBlrel. 04, Last sequence update)		
DT	01-NOV-1999	(TREMBlrel. 12, Last annotation update)		
DE	LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 9.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Carnivora; Hominoidea; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 97272273.			
RA	SCRATON G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,			
RA	MCMICHAEL A.J., BELL J.I.;			
RT	"LARD: a new lymphoid-specific death domain containing receptor			
RT	regulated by alternative pre-mRNA splicing."			

Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL: U94510; AAC51315.1; -  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PFAM: PF00531; death.1.  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR SEQUENCE 380 AA; 41192 MW; 17C92A14 CRC32;

Query Match 73.6%; Score 2403; DB 4; Length 380;  
 Best Local Similarity 89.1%; Pred. No. 0.00e+00;  
 Matches 369; Conservative 4; Mismatches 4; Indels 37; Gaps 1;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63  
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74  
 Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 123  
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 134  
 Db 124 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 183  
 135 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 194  
 Db 184 LGSCPERCAAVCGMRQ-----NEAGMEA 206  
 195 LGSCPERCAAVCGMRQMFVQVLLAGLVPLLLGATLTYTRHGWPKPLVTADAEAMEA 254  
 Db 207 LTPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTPGYPTQALCPQVTSWMDQL 266  
 255 LTPPATHLSPDLSAHTLLAPDSSEKICTVQLVGNSTPGYPTQALCPQVTSWMDQL 314  
 Db 267 PSRSLGPAAPRTSPSPGSPAMLOPQPOLYDMADAVARRKKEVRLGLREATEIA 326  
 315 PSRSLGPAAPRTSPSPGSPAMLOPQPOLYDMADAVARRKKEVRLGLREATEIA 374  
 Db 327 VEVEIGRFRDQYEMLRKMRQOPAGIGAVYALERMGLDGCVEDLSRLQRP 380  
 375 VEVEIGRFRDQYEMLRKMRQOPAGIGAVYALERMGLDGCVEDLSRLQRP 428  
 QY

RESULT 5  
 ID 000276 PRELIMINARY; PRT; 253 AA.  
 AC 000276;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97272273.  
 RA SCREATOR G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,  
 RA MCMICHAEL A.J., BELL J.I.;  
 RT "LARD: a new lymphoid-specific death domain containing receptor  
 regulated by alternative pre-mRNA splicing."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL: U94503; AAC51308.1; -  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR SEQUENCE 253 AA; 26934 MW; A21C863E CRC32;

Query Match 45.8%; Score 1497; DB 4; Length 253;  
 Best Local Similarity 95.5%; Pred. No. 0.00e+00;  
 Matches 190; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63  
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74  
 QY

Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 123  
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 134  
 Db 124 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 183  
 135 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 194  
 Db 184 LGSCPERCAAVCGMRQSW 202  
 195 LGSCPERCAAVCGMRQMFV 213  
 QY

RESULT 6  
 ID 014866 PRELIMINARY; PRT; 277 AA.  
 AC 014866;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
 DE SOLUBLE DEATH RECEPTOR 3 BETA.  
 GN DR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MAZOCCHA K., RIBEIRO P., RENARD N., CHARLOT C., COIFFIER B.,  
 RA SALES G.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF026071; AAB82288.1; -  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR SEQUENCE 277 AA; 29111 MW; 06E165C7 CRC32;

Query Match 41.1%; Score 1343; DB 4; Length 277;  
 Best Local Similarity 95.5%; Pred. No. 1.19e-271;  
 Matches 171; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 4 RPRGCAVAALLLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 63  
 15 RGSAPAPVQALLVLLGARAAGGTRSPRCDAGDFHKKIGLFCRCGCPAGHYLKAPCTE 74  
 Db 64 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 123  
 75 PCGNSTCLVCPQDPTFLAMENHNHNSCARCOACDEQASQVALENCASAVADTRGCGKPGMFV 134  
 Db 124 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 182  
 135 ECQVSQCVCSSPFYCPQCLDGCALHRRHRLCSRRDTCGTCIPGFYEHGDGVCSCPTST 193  
 QY

RESULT 7  
 ID 000278 PRELIMINARY; PRT; 234 AA.  
 AC 000278;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, last annotation update)  
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 7.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97272273.  
 RA SCREATOR G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,  
 RA MCMICHAEL A.J., BELL J.I.;  
 RT "LARD: a new lymphoid-specific death domain containing receptor  
 regulated by alternative pre-mRNA splicing."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL: U94508; AAC51313.1; -  
 DR PFAM: PF00531; death.1.  
 DR SEQUENCE 234 AA; 25373 MW; 272FD3C9 CRC32;

Query Match 40.7%; Score 1329; DB 4; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2,14e-268;  
 Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 53 ADEGMALPPATHTSPDASHTLAPDPSSSEKICTVOLVGNWMTPGYPTOALCPQ 112  
 |||||  
 QY 247 ADEGMALPPATHTSPDASHTLAPDPSSSEKICTVOLVGNWMTPGYPTOALCPQ 306  
 |||||

Db 113 VTMWMDLPRAALCPAAPTLPSPSPAGSPAMMLQPGPOLYDVADAVPARMKKEFVRLTG 172  
 |||||  
 QY 307 VTMWMDLPRAALCPAAPTLPSPSPAGSPAMMLQPGPOLYDVADAVPARMKKEFVRLTG 366

Db 173 LREAEIFAVEVEIGRFDOOYEMLKRRQOQPAGLGAVYALERMGLDGCVEDLRSRLO 232  
 |||||  
 QY 367 LREAEIFAVEVEIGRFDOOYEMLKRRQOQPAGLGAVYALERMGLDGCVEDLRSRLO 426

Db 233 GP 234  
 |||||  
 QY 427 GP 428

RESULT 8  
 ID 000277; PRELIMINARY; PRT: 126 AA.  
 AC 000277;  
 DT 01-JUL-1997 (TREMBLrel. 04, Created)  
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
 DE LYMPHOCYTE ASSOCIATED RECEPTOR OF DEATH 6.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 97272273.  
 RA SCRETON G.R., XU X.N., OLSEN A.L., COMPER A.E., TAN R.,  
 RA MICHAEL A.J., BELL J.I.;  
 RA "IARD: a new lymphoid-specific death domain containing receptor  
 RT regulated by alternative pre-mRNA splicing";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).  
 DR EMBL; U94507; AAC51312.1; -;  
 SQ SEQUENCE 126 AA; 13349 MW; BAB4851A CRC32;

Query Match 14.3%; Score 467; DB 4; Length 126;  
 Best Local Similarity 92.2%; Pred. No. 2.63e-72;  
 Matches 59; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Db 48 CRGCPA-ASQVLENCASVADTRCGCKRGWVEYECQVSSSPYCPCLDGCALHRT 106  
 |||||  
 QY 103 CQACDEQASQVLENCASVADTRCGCKRGWVEYECQVSSSPYCPCLDGCALHRT 162

Db 107 RLIC 110  
 |||||  
 QY 163 RLIC 166

RESULT 9  
 ID 019131; PRELIMINARY; PRT: 471 AA.  
 AC 019131;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE Tumor NECROSIS FACTOR-RECEPTOR I.  
 GN TNF-R1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 OC Bovinae; Bos.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-AORTA;  
 RA LEE E.-K., TAYLOR M.J., KEHLI M.E.;  
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.

DR EMBL; U90937; AAB65143.1; -;  
 DR HSSP; P19438; 11NR.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PFAM; PF00531; death; 1.  
 DR PFAM; PF00020; TNFR\_c6; 3.  
 SQ SEQUENCE 471 AA; 51367 MW; 1D60FF4A CRC32;

Query Match 8.3%; Score 272; DB 6; Length 471;  
 Best Local Similarity 30.0%; Pred. No. 2.91e-31;  
 Matches 128; Conservative 79; Mismatches 169; Indels 51; Gaps 34;

Db 40 RESPCP-OGKYNHPONSTICCTCKHGYLYNDGPGPRDTCRCVACGTYALENHLRR 98  
 |||||  
 QY 40 RSPRDCAGDF-HKKGIFCCRCGCPAGHYLKAFTPCGNSCYLCPODFTFLAMENHNS 98

Db 99 -CLSSRRDEMFQVEIPCVVDRTVCGCKRQVREW-GE-TGFRCLNCSLCPN-GTV 154  
 |||||  
 QY 99 ECARCOACDEQASQVLENCASVADTRCGCKRGWVEYECQVSSSPYCPCLDGCAL 158

Db 155 NIPCO---ERODTIC-HCHMGFELKACISCHDCNKKECEKICPTPRSTGKDSODPTT 210  
 |||||  
 QY 159 HRTRLCSRRDTCGCTLPRTYEHGDCVSCPTSLGCPRCAA-VC-GW-RQMFWYQ 215

Db 211 VLLPLVIFGLCLASFAVAVIACRYQRMKPKLYSTICGOSTLVKGEPELVAPGPNPT 270  
 |||||  
 QY 216 VLLAGLVV-PL-LIG-ATLTYR-HCWPBK--PLV---T-ADEAGMALP-P---PA 260

Db 271 TTICSSSPSSSPVSIPIPIYISCDRNFQAVASPSSETAPPHLKAPTLPGPASTHLCPT 330  
 |||||  
 QY 261 THL--SPDASHTLAP-DSEK--ICTVOLVGNWMTPGYPTOALC-PQYTSW-DQ 313

Db 331 GPASTHLCPTGPASTHLCPTVQKWEASAPADOLADPATLYAVDVGPSRKL 390  
 |||||  
 QY 314 -LPSRA-L---GPAAPTL-SP-----ESPA-GSPAMMLQPGPOLYDVADAVPARMKKEF 361

Db 391 VRLGISEHEIRLENGRHIREAOYSMLAMRRRTPREATLELGLVLDMDLGLT 450  
 |||||  
 QY 362 VTLGIREAEIFAVEVEIGR-FRDOOYEMLKRRQOQ---AGLAVYALERMGLDGCV 417

Db 451 ENIEEAL 457  
 |||||  
 QY 418 EDLRSRL 424

RESULT 10  
 ID 097491; PRELIMINARY; PRT: 327 AA.  
 AC 097491;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)  
 DE FAS PROTEIN.  
 GN FAS.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;  
 OC Caprinae; Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-LYMPHOCYTE;  
 RA TAKAGI M., TAKAHASHI H., KABEYA H., OHASHI K., SUGIMOTO C., ONUMA M.;  
 RT "Cloning of sheep fas antigen";  
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AB011671; BAA37093.1; -;  
 DR HSSP; P25445; 1DDF.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
 SQ SEQUENCE 327 AA; 36928 MW; 67261BB8 CRC32;

Query Match 6.7%; Score 218; DB 6; Length 327;  
 Best Local Similarity 30.2%; Pred. No. 1.13e-20;  
 Matches 32; Conservative 23; Mismatches 44; Indels 7; Gaps 5;

Db 56 LRCCGCPGPKRKNCKCKRDGMPCEVLCSEGEYTD-KSHSDKICRCVCDENGLGV 114  
 |||||

OY 56 LFCRCGCPAGHYLKAPCTEPCGNSSTCLVCPQ-DTFLAMENHNHNSCARQACDEQASOVA 114  
DB 115 EHNCSTRONTKCRCKSNF--CNSSPCEHCNP--CTTC-EHGLEK 155  
OY 115 LENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGALHR 160

RESULT 11  
ID 09Y606 PRELIMINARY: PRT: 616 AA.  
AC 09Y606:  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
DE RECEPTOR ACTIVATOR OF NUCLEAR FACTOR-KAPPA B.  
GN RANK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE: 98032977.  
RA ANDERSON D.M., MARASROVSKY E., BILLINGSLEY W.L., DOUGALL W.C.,  
RA TOMESKO M.E., KOX E.R., TEEPE M.C., DUBOSE R.F., COSMAN D.,  
RA GALBERT L.;  
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
RT and dendritic-cell function."  
RL Nature 390:175-179(1997)  
DR EMBL: AF018253; AAB86809.1; -.  
KW Receptor.  
SQ SEQUENCE 616 AA; 66033 MW; 6AF398F8 CRC32;

Query Match 6.5%; Score 213; DB 4; Length 616;  
Best Local Similarity 31.0%; Pred. No. 1,01e-19;  
Matches 49; Conservative 29; Mismatches 65; Indels 15; Gaps 14;

DB 15 LLLCALLARLQVALIAPCTSEKHYEH-LGR-CCNKCEPKYMSKCTTT-SDSVCLPC 71  
OY 26 LLLVLLGARAAGGTR-SPRCDCAGDFHKKIGLFCRCGCPAGHYLKAPCTEPCGNSSTCLVC 84  
DB 72 GPDEYLDMS-NEEDK-CLHKVVDITGKALVAVVAGNSTTTRRACCTAG-TWMSDCECCR 128  
OY 85 PDOTFL-AMENHNHNSCARQACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCVS 143  
DB 129 RNT-ECAPGL-GA-O-HPLQL-NK-DTVCKPLAGYF 159  
OY 144 SSPFYCQPCLDGALHRHRLCSDRDTCGTCLPGFY 181

RESULT 12  
ID 09Y530 PRELIMINARY: PRT: 189 AA.  
AC 09Y530:  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DUTHIE S., NASIR L., ARGYLE D.J., ECKERSALL P.D.;  
RT "Canine tumor necrosis factor receptor, partial cds."  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF013955; AAD01516.1; -.  
DR HSSP: P19438; 1TNR.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
KW Receptor.  
FT NON\_TER 189  
SQ SEQUENCE 189 AA; 21324 MW; 2AA93BEF CRC32;

Query Match 6.4%; Score 210; DB 6; Length 189;  
Best Local Similarity 31.8%; Pred. No. 3.74e-19;

Matches 47; Conservative 23; Mismatches 66; Indels 12; Gaps 8;  
DB 44 CPOGTYHPDDSDTCTCHGTYLYNDGPGGLDTRCECNGTFTASENHLR-QCLSC 102  
OY 46 CA-GDF-HKKIGLFCRCGCPAGHYLKAPCTEPCGNSSTCLVCPQDFTFLAMENHNHNSCARC 103  
DB 103 SKCRKNMVEISPCTVYRDVCGCRKN--OYRFY--SEPTLFCGNNCSLC--LNGTVQ 155  
OY 104 QACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGALHRHTR 163  
DB 156 ISCOEKONTIC-TCHAGFFLRHEHCVSC 182  
OY 164 LLC-SRDPTDGTCLPGFYEHGDCGVSC 190

RESULT 13  
ID 095185 PRELIMINARY: PRT: 189 AA.  
AC 095185:  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR P60 (FRAGMENT).  
GN TNFR-1.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA DUTHIE S., NASIR L., ECKERSALL P.D.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U72344; AAB95089.1; -.  
DR HSSP: P19438; 1EXT.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
DR PFAM: PF00020; TNFR\_C6; 3.  
FT NON\_TER 189  
SQ SEQUENCE 189 AA; 21420 MW; 687732D2 CRC32;

Query Match 6.3%; Score 206; DB 6; Length 189;  
Best Local Similarity 31.8%; Pred. No. 2.12e-18;  
Matches 49; Conservative 24; Mismatches 67; Indels 14; Gaps 11;

DB 40 RAIPCP-OGKTYHPDINSICCTKCHGTYLYNDGPGGLDTRCECNGTFTASENHLR- 97  
OY 40 RSPDCDQGD-CHKIGLFCRCGCPAGHYLKAPCTEPCGNSSTCLVCPQDFTFLAMENHNHNS 98  
DB 98 QCLSCSKCRKNMVEISPCTVYRDVCGCRK---N-OY-RYWSETHF-O-CLNCSLC 149  
OY 99 ECARQACDEQASOVALENCASAVADTRCGCKPGWFEVCQVSCVSSPFYCQPCLDGCA- 157

DB 150 LNTGVQISCKETONTVC-TCHAGFFLRHEHCVSC 182  
OY 158 LHRHRLCS-RDPTDGTCLPGFYEHGDCGVSC 190

RESULT 14  
ID 09XS60 PRELIMINARY: PRT: 263 AA.  
AC 09XS60:  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)  
DT 01-NOV-1999 (TREMBLrel. 12, last annotation update)  
DE PAS ANTIGEN SPLICED VARIANT.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA ISONO T., TANBE Y., NAGANO Y., SETO A.;  
RT "Splicing and allelic variation in the rabbit Pas antigen gene."  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB021297; BAA78429.1; -.  
SQ SEQUENCE 263 AA; 30374 MW; 43BF129F CRC32;

Query Match 6.2%; Score 202; DB 6; Length 263;





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 WISE (TM)  
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MSrch\_PP protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Jul 25 22:20:00 2000; Maspar time 15.22 Seconds  
 871.530 Million cell updates/sec  
 Tabular output not generated.

Title: >US-09-314-889-2  
 Description: (1-428) from US09314889.pep  
 Perfect Score: 3267  
 Sequence: 1 MEETQGEAFRGQLRGESAA.....ERMGLDGCVEDLRSLRQGP 428

Scoring table: PAM 150  
 GAP 11

Searched: 85661 segs, 30989116 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 48.842; Variance 83.135; scale 0.588

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description	Pred. No.
1	3118	95.4	417	1	WSL1_HUMAN	0.00e+00
2	407	12.5	455	1	TNRI_HUMAN	9.43e-63
3	399	12.2	454	1	TNRI_MOUSE	6.00e-61
4	388	12.2	461	1	TNRI_PIG	1.01e-60
5	383	11.7	461	1	TNRI_RAT	2.35e-57
6	278	8.5	332	1	FASL_PIG	2.14e-34
7	213	6.5	323	1	FASL_BOVIN	5.49e-21
8	211	6.5	324	1	FASL_RAT	1.37e-20
9	204	6.2	327	1	FASL_MOUSE	3.32e-19
10	190	5.8	335	1	FASL_HUMAN	1.77e-16
11	182	5.6	326	1	VT2_MYVL	6.00e-15
12	179	5.5	349	1	VC22_VARV	2.22e-14
13	177	5.4	260	1	CD27_HUMAN	5.28e-14
14	165	5.1	271	1	OX40_RAT	8.94e-12
15	167	5.1	272	1	OX40_MOUSE	3.84e-12
16	168	5.1	461	1	TNRC_HUMAN	2.51e-11
17	164	5.0	325	1	VT2_SPYKA	1.36e-11
18	159	4.9	277	1	CD40_HUMAN	1.10e-10
19	160	4.9	435	1	TNRC_HUMAN	7.29e-11
20	161	4.9	474	1	TNRC_HUMAN	4.80e-11
21	158	4.8	250	1	CD27_MOUSE	1.67e-10
22	157	4.8	415	1	TNRC_MOUSE	2.53e-10
23	153	4.7	656	1	RIP_MOUSE	1.31e-09

24	146	4.5	416	1	NGFR_CHICK	LOW-AFFINITY NERVE GRO	2.24e-08
25	139	4.3	427	1	NGFR_HUMAN	LOW-AFFINITY NERVE GRO	3.59e-07
26	134	4.1	671	1	RIP_MOUSE	SERINE/THREONINE PROTE	2.50e-06
27	131	4.0	425	1	NGFR_RAT	LOW-AFFINITY NERVE GRO	7.88e-06
28	124	3.8	3635	1	LMNA_MOUSE	LAMININ ALPHA-5 CHAIN	1.08e-04
29	116	3.6	799	1	ITB5_HUMAN	INTEGRIN BETA-5 PRECUR	1.96e-03
30	114	3.5	277	1	OX40_HUMAN	OX40L RECEPTOR PRECURS	3.96e-03
31	114	3.5	1247	1	NIDO_HUMAN	NIDOGEN PRECURSOR (ENT	3.96e-03
32	110	3.4	269	1	CD40_BOVIN	CD40L RECEPTOR PRECURS	1.58e-02
33	110	3.4	289	1	CD40_MOUSE	CD40L RECEPTOR PRECURS	1.58e-02
34	111	3.4	655	1	ITB5_PAPCY	INTEGRIN BETA-5 (FRAGM	1.12e-02
35	111	3.4	1607	1	LMG1_MOUSE	LAMININ GAMMA-1 CHAIN	1.12e-02
36	112	3.4	1609	1	LMG1_HUMAN	LAMININ GAMMA-1 CHAIN	7.95e-03
37	108	3.3	103	1	VA53_VACC	PROTEIN A53.	3.12e-02
38	108	3.3	103	1	VA53_VACCV	PROTEIN A53.	3.12e-02
39	109	3.3	400	1	LMH_HTRME	LAMININ B-CHAIN (FRAGM	2.22e-02
40	108	3.3	612	1	OCTC_RAT	PEROXISOMAL CARINITINE	3.12e-02
41	108	3.3	647	1	GAG_SFVL	GAG POLYPROTEIN (CORE	3.12e-02
42	107	3.3	883	1	PGCB_MOUSE	BREVICAN CORE PROTEIN	4.37e-02
43	108	3.3	1245	1	NIDO_MOUSE	NIDOGEN PRECURSOR (ENT	3.12e-02
44	109	3.3	1789	1	LMH1_DROME	LAMININ BETA-1 CHAIN P	2.22e-02
45	109	3.3	3707	1	PGBM_MOUSE	BASEMENT MEMBRANE-SPEC	2.22e-02

## ALIGNMENTS

RESULT 1 STANDARD; PRT; 417 AA.  
 ID WSL1\_HUMAN  
 AC Q93038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;  
 AC Q99830;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-  
 DE MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)  
 DE (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED  
 DE RECEPTOR OF DEATH) (LARD).  
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.  
 RC TISSUE=LIMPHOID.  
 RX MEDLINE; 97088617.  
 RA Kiltson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
 RA Grinham C.J., Brown R., Farrow S.N.;  
 RT "A death-domain-containing receptor that mediates apoptosis.";  
 RN Nature 384:372-375(1996).  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=UMBILICAL VEIN ENDOTHELIAL CELLS;  
 RX MEDLINE; 97081063.  
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
 RA Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
 RT "Signal transduction by DR3, a death domain-containing receptor  
 RT related to TNFR-1 and CD95.";  
 RN Science 274:990-992(1996).  
 RP [3]  
 RP SEQUENCE FROM N.A.  
 RA Degli-Esposti M.A., Din W.S., Gosman D., Smith C.A., Goodwin R.G.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART;  
 RX MEDLINE; 97148200.  
 RA Masters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;  
 RT "Apo-3, a new member of the tumor necrosis factor receptor family,  
 RT contains a death domain and activates apoptosis and NF-kappa-B.";  
 RN Curr. Biol. 6:1669-1676(1996).  
 RP [5]  
 RP SEQUENCE FROM N.A.

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RX MEDLINE: 972712273.
RA RA Screation G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R.,
RA McMichael A.J., Bell J.I.;
RT "LARD: a new lymphoid-specific death domain containing receptor
RT regulated by alternative pre-mRNA splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RN [6]
RF SEQUENCE OF 4-417 FROM N.A.
RC TISSUE-BRAIN, AND FETAL LUNG;
RX MEDLINE: 97205335.
RA Bodmer J.-L., Burns K., Schneider P., Hofmann K., Steiner V.,
RA Thome M., Bornand T., Hahne M., Schroeter M., Wilson A., French L.E.,
RA Brownling J.L., McDonald H.R., Tschopp J.;
RT "TRAMP, a novel apoptosis-mediating receptor with sequence homology
RT to tumor necrosis factor receptor 1 and Fas(Apo-1/CD95).";
RN Immunity 6:79-88(1997).
RP [7]
RP SEQUENCE OF 7-417 FROM N.A.
RC TISSUE-BRAIN;
RA Chaudhary P.M., Hood L.E.;
RT Submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.
CC -I- FUNCTION: INDUCES APOPTOSIS AND ACTIVATES NUCLEAR FACTOR KAPPA-B
CC (NF-KAPPA-B). DIRECTLY INTERACTS WITH TRADD ADAPTOR MOLECULE. MAY
CC PLAY A ROLE IN REGULATING LYMPHOCYTE HOMEOSTASIS.
CC -I- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH
CC THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNFR1 RECEPTOR TO
CC ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES. APOPTOSIS AND
CC NF-KAPPA B SIGNALING.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -I- ALTERNATIVE PRODUCTS: THREE ISOFORMS: WSL-1/LARD-1A (SHOWN HERE),
CC WSL-S1/LARD-3 AND WSL-S2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND
CC LYMPHOCYTES. DETECTED IN LYMPHOCYTE-RICH TISSUES SUCH AS THYMUS,
CC COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
CC -I- PTM: GLYCOSYLATED (PROBABLE).
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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DR EMBL: Y09392; CAA70561.1; -
DR EMBL: Y09392; CAA70559.1; -
DR EMBL: Y09392; CAA70560.1; -
DR EMBL: U72763; AAC50819.1; -
DR EMBL: U83599; AAB41434.1; -
DR EMBL: U83600; AAB41435.1; -
DR EMBL: U78029; AAB40918.1; -
DR EMBL: U74611; AAB39714.1; -
DR EMBL: U94501; AAC51306.1; -
DR EMBL: U94504; AAC51309.1; -
DR EMBL: U75380; AAC51192.1; -
DR EMBL: U75381; AAC51193.1; -
DR EMBL: U83597; AAB41432.1; -
DR HSSP: P19438; ITNR.
DR MIM: 603366; -
DR PFAM: PF00020; TNFR_C6; 2.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Apoptosis; Alternative splicing; Transmembrane; Signal;
Repeat.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 417 WSL-1 PROTEIN.
FT DOMAIN 25 199 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 200 220 POTENTIAL.
FT DOMAIN 223 417 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 334 192 4 X TNFR-CYS.

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FT	REPEAT	34	71	TNFR-CYS 1.
FT	REPEAT	116	115	TNFR-CYS 2.
FT	REPEAT	116	163	TNFR-CYS 3.
FT	REPEAT	164	192	TNFR-CYS 4.
FT	DOMAIN	332	413	DEATH DOMAIN.
FT	CARBOHYD	67	67	POTENTIAL.
FT	CARBOHYD	106	106	POTENTIAL.
FT	VARSPLIC	182	218	STIGSCERCACAAVCGMROMFWOVLVLAGVLPULLGA -> VLGAGAGMPCGPPAGPHDHLIIPPLASQAGYCR (IN ISOFORM WSL-S1).
FT	VARSPLIC	219	417	MISSING (IN ISOFORM WSL-S1).
FT	VARSPLIC	200	253	MENVOVLVLAGVLPULLGATLTYTRHCWPKRYTADAG MEATLTPPAHLS -> SRACAGNARKRTGMDZGEABEG NHPTPTFCQSSSRCSRWALMSBSCGPP (IN ISOFORM WSL-S2).
FT	VARSPLIC	254	417	MISSING (IN ISOFORM WSL-S2).
FT	MUTAGEN	354	354	L-2A: SUPPRESSES HOMODIMERIZATION, TNFR1 INTERACTION, AND APOPTOSIS INDUCTION.
FT	MUTAGEN	356	356	L-2A: SUPPRESSES HOMODIMERIZATION, AND TNFR1 INTERACTION.
FT	MUTAGEN	373	373	D-2A: SUPPRESSES HOMODIMERIZATION, AND TNFR1 INTERACTION.
FT	CONFLICT	4	6	RPR -> AAA (IN REF. 6).
FT	CONFLICT	60	60	P -> H (IN REF. 7).
FT	CONFLICT	167	167	P -> L (IN REF. 6 AND 7).
FT	CONFLICT	312	312	A -> R (IN REF. 1).
FT	CONFLICT	370	370	R -> L (IN REF. 1).
FT	CONFLICT	381	381	R -> H (IN REF. 1).
SQ	SEQUENCE	417 AA;	45385 MM; 5226319PFD846706 CRC64;	
Query Match 95.4%; Score 3118; DB 1; Length 417;				
Matches 407; Similarity 98.3%; Pred. No. 0.00e+00;				
Conservative 3; Mismatches 4; Indels 0; Gaps 0				
Db	4	RRGCAAAVAAALLVLLGARAAGGTRSPRCDCAGDFHKIGLFCRCGCPAGHYLKAPCTE	63	
QY	15	RGESAAVPQALLVLLGARAAGGTRSPRCDCAGDFHKIGLFCRCGCPAGHYLKAPCTE	74	
Db	64	PGNSTCLVCPQDPTFLAENHNHNSCACQACDBASOVALIENCSAVNDFGCGKPGMEV	123	
QY	75	PGNSTCLVCPQDPTFLAENHNHNSCACQACDBASOVALIENCSAVNDFGCGKPGMEV	134	
Db	124	ECQVSCQVSSSFYEQCPCLDCGALHRHRLRLCSRBDTCGTLDPGYEHGDCVSCPTST	183	
QY	135	ECQVSCQVSSSFYEQCPCLDCGALHRHRLRLCSRBDTCGTLDPGYEHGDCVSCPTST	194	
Db	184	LGSCEBCAACVGMROMFWOVLVLAGVLPULLGATLTYTRHCWPKRYTADAGMEA	243	
QY	195	LGSCEBCAACVGMROMFWOVLVLAGVLPULLGATLTYTRHCWPKRYTADAGMEA	254	
Db	244	LTPPATHLSPDASHNTLAPDSSSEKICTQVLVNSMTPGYPETQALCPQVYMSDQL	303	
QY	255	LTPPATHLSPDASHNTLAPDSSSEKICTQVLVNSMTPGYPETQALCPQVYMSDQL	314	
Db	304	PSRALGPAAAPLTPSPSPAGSPAMMLQCPQLYDVMDAVPARMKKEFVRTIGLRAETEA	363	
QY	315	PSRALGPAAAPLTPSPSPAGSPAMMLQCPQLYDVMDAVPARMKKEFVRTIGLRAETEA	374	
Db	364	VEVEIGRFDDQOYEMLKRMROOQPGLAGVYALERMGIDGVEDLRSRLRQGP	417	
QY	375	VEVEIGRFDDQOYEMLKRMROOQPGLAGVYALERMGIDGVEDLRSRLRQGP	428	
RESULT				
AC	TNRL HUMAN	STANDARD:	PRT;	455 AA.
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 1) (TNF1) (P60) (TNF-R1) (P55) (CD120A).			
DE	TNFRSF1A OR TNFR1 OR TNFR4			
OS	Homo sapiens (Human).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthetia; Primates; Catarrhini; Homiidae; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-PLACENTA;  
RX MEDLINE: 90235285.  
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,  
RA Getanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V.,  
RT "Molecular cloning and expression of a receptor for human tumor  
RT necrosis factor.";  
RL Cell 61:361-370(1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 90235284.  
RA Loetscher H., Pan Y.-C.E., Lahn H.-W., Gentz R., Brockhaus M.,  
RA Tabuchi H., Lesslauer W.;  
RT "Molecular cloning and expression of the human 55 kd tumor necrosis  
RT factor receptor.";  
RL Cell 61:351-359(1990).  
RN [3]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
RX MEDLINE: 91006021.  
RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,  
RA Aderka D., Holtmann H., Wallach D.;  
RT "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
RT for the type I TNF-R, cloned using amino acid sequence data of its  
RT soluble form, encodes both the cell surface and a soluble form of the  
RT receptor.";  
RL EMBO J. 9:3269-3278(1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91090841.  
RA Himmeler A., Maurer Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
RT "Molecular cloning and expression of human and rat tumor necrosis  
RT factor receptor chain (p60) and its soluble derivative; tumor  
RT necrosis factor-binding protein.";  
RL DNA Cell Biol. 9:705-715(1990).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX TISSUE-PLACENTA;  
RX MEDLINE: 91017509.  
RA Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;  
RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
RT expression of recombinant soluble TNF-binding protein.";  
RL Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 92250049.  
RA Fuchs P., Strelh S., Dworzak M., Himmeler A., Ambros P.F.;  
RT "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
RT localization to chromosome 12p13.";  
RL Genomics 13:219-224(1992).  
RN [7]  
RP SEQUENCE OF 41-45.  
RX MEDLINE: 90110215.  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
RT urine. Evidence for immunological cross-reactivity with cell surface  
RT tumor necrosis factor receptors.";  
RL J. Biol. Chem. 265:1531-1536(1990).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
RX MEDLINE: 931258809.  
RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
RA Broger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
RT beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RX MEDLINE: 97094982.  
RA Naimuth J.H., Devine T.O., Khono H., Sprang S.R.;

RT	Factor receptor."	
RL	Structure 4:1251-1262(1996).	
CC	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD	
CC	RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING	
CC	AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)	
CC	PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE	
CC	SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE	
CC	PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF	
CC	NONCYCLOidal TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION	
CC	OF THE ACID SPUNGOMYELINASE.	
CC	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO	
CC	HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS	
CC	PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY	
CC	WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING	
CC	PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO	
CC	TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX	
CC	ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND	
CC	NF-KAPPA B SIGNALING.	
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.	
CC	-1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO	
CC	THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH	
CC	NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.	
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.	
CC	-1- DATABASE: NAME=PRO; NOTE=CD guide CD120a entry;	
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm"	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; X5513; CA939021.1; -	
DR	EMBL; M33294; AAA03210.1; -	
DR	EMBL; M58286; AAA36753.1; -	
DR	EMBL; M63121; AAA36754.1; -	
DR	EMBL; M75866; AAA61201.1; -	
DR	EMBL; M75866; AAA61201.1; JOINED.	
DR	EMBL; M75865; AAA61201.1; JOINED.	
DR	EMBL; M60275; AAA36756.1; -	
DR	EMBL; A21522; CA01558.1; -	
DR	PIR; A34899; G0HUT1.	
DR	PIR; A35010; A35010.	
DR	PIR; S12057; S12057.	
DR	PIR; A38208; A38208.	
DR	PDB; 1TNR; 3I-JUL-94.	
DR	PDB; 1NCF; 07-DEC-95.	
DR	PDB; TEXT; 1I-JAN-97.	
DR	MM; 191190; -	
DR	PFAM; PF00020; TNFR_c6; 4.	
DR	PROSITE; PS00531; death; 1.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	
DR	PROSITE; PS00505; TNFR_NGFR_2; 3.	
DR	PROSITE; PS50017; DEATH.DOMAIN; 1.	
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis;	
KW	3d-structure.	
FT	SIGNAL	21
FT	CHAIN	22 455
FT	CHAIN	41 291
FT	DOMAIN	22 211
FT	TRANSMEM	212 234
FT	DOMAIN	235 455
FT	DOMAIN	43 196
FT	REPEAT	43 82
FT	REPEAT	83 125
FT	REPEAT	126 166
FT	REPEAT	167 196
FT	DOMAIN	338 348
FT	DOMAIN	356 441
FT	DISULFID	44 58
CC	TUMOR NECROSIS FACTOR RECEPTOR 1.	
CC	TUMOR NECROSIS FACTOR BINDING PROTEIN 1.	
CC	EXTRACELLULAR (POTENTIAL).	
CC	POTENTIAL.	
CC	CYTOPASMIC (POTENTIAL).	
CC	4 X TNFR-CYS.	
CC	TNFR-CYS 1.	
CC	TNFR-CYS 2.	
CC	TNFR-CYS 3.	
CC	TNFR-CYS 4.	
CC	N-SMASE ACTIVATION DOMAIN (NSD).	
CC	DEATH DOMAIN.	





FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 190 BY SIMILARITY.  
 FT DISULFID 185 194 BY SIMILARITY.  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 145 145 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 SQ SEQUENCE 461 AA; 50696 MW; CD72361BC60C9D43 CRC64;

Query Match 12.2%; Score 398; DB 1; Length 461;  
 Best Local Similarity 32.3%; Pred. No. 1,01e-60;  
 Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

Db 33 HRPDREKREELCQGKSHQNRISICCTCKHKYTLINDCLGPDLDIDDCRCNDGNTFTAS 92  
 36 QGGTRSR-CDCA-GDF-HKRGLECCRCGPAGHYLAAPTEPCGNSYCLVCPDPTFLAW 92  
 93 ENHL-TQCLSCSKCRSMSCOVEISPTVDRDTCVGCGRKN--QYR--KY-MSETLF-Q-C 143  
 93 ENHNSCARCQACDEQASQVALNCASAVADTRCGCKPQWVEQVSCVSSSEFYCQPC 152  
 144 LNC-SLCPNGTVLPCLKEKODTICN-CHSGFELDKECVSCVCKNADCKNLCPATSETR 201  
 153 LDGALHRR-T-RLLC-SRBDTCGTCLPGYEHGDCVSCPTSLGSCPERCAVCGMR 209  
 202 NDRQDTTTLPLVIFVIFGLCLAFVYGLACRQR-WKPKLYSLICKSTPVKEGEP 260  
 210 QMW--VOYLLA-----GLVPLLLGATLTYYTHCWPKR--PLV----TA-DEAGMEA 254  
 261 LAFAPSGPTTFSPSPPTTFSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 320  
 255 L-TFP---PATHSLPDS-AHTL-LAPDSESEKICTQVLVNSMTP---GVPENGEALCP 305  
 321 QGAPILPMPASTVPPLPKWGSASHASAPQADADPATLYAVDGPPTPKMEF 380  
 306 QVTWSMQLP-SRALGPAAAPTL--SPESPASPMMLQPPGO-LYDWDADVAPARRMEF 361  
 381 VRRGLSEHETERELNGRCLEAOXSMLAEWRRTRSRREATTELLGSVRDMLGLCL 440  
 362 VRTGLREALEAEVEVEIGR-FRDOYEMLRMRQO--QP-AGLAGVYALALERMGLDGV 417  
 441 EDIEEAL-RGP 450  
 418 EDLSRLQGRCP 428

RESULT 5  
 ID TNRI\_RAT STANDARD; PRT; 461 AA.  
 AC P22934;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91090841.  
 RA Himmeler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 RT factor receptor chain (p60) and its soluble derivative, tumor  
 RT necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFS, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M63122; AAA42256.1; -;  
 CC PIR; B36555; B36555.  
 DR HSSP; P19438; TNFR.  
 DR PFAM; PF00020; TNFR\_c6; 4.  
 DR PFAM; PF00531; death; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 KM Receptor; Transmembrane; Glycoprotein; Repeat; signal; Apoptosis.  
 FT SIGNAL 1 21  
 FT CHAIN 1 21  
 FT DOMAIN 22 211  
 FT DOMAIN 22 211  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 461  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 123  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 344 354  
 FT DOMAIN 363 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 201 201  
 SQ SEQUENCE 461 AA; 50696 MW; EB23C05450FBD202 CRC64;

Query Match 11.7%; Score 383; DB 1; Length 461;  
 Best Local Similarity 29.8%; Pred. No. 2,35e-57;  
 Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;

Db 35 GDRKRDNLCPQGYAHPRNNSICCTCKHKYTLVSDCPSPGOETVCEVCDKGTPTASON 94  
 38 GTRSPRCD-CA-GDF-HKRGLECCRCGPAGHYLAAPTEPCGNSYCLVCPDPTFLAW 94  
 95 H-VROCLSKTCKRKEMFQYVETSPCKADMDVCGCKKNQGRYLSHHPQCYDSCPENGT 153  
 95 HNSSEARQACDEQASQVALNCASAVADTRCGCKPQWVEQVSCVSSSEFYCQPC 150  
 154 VTPPCKE-KONTVCNCHAEFLSGNCTPCSHCKKNOCKKILCLPVAVTNTPDQSGTAV 212  
 151 PCLDGCALHRRHRLCLSRDIDCGT-CLP-GYEHGDCVS-C-PISTLGSCEGCAAVC 206  
 213 LPLVIFGLCLFFICISLLCRYPQWRPRVYSIICRDSAPVKEVGEGLVTKPLTPAST 272

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OY 207 GWRMFWGV-LLAGLVPL--LGATLTYTRH-CMPKPLVADACM--EALTPPPA 260
DB 273 PAFSPNPGNPLTGSTTRFRSHVSTPISPFGRSMNHNPVPPREVPTO-G-A-DP 329
OY 261 THLSPLDS-AHTL-LAP-PDSSSEKICTYQL--V-GNS-WTPGYPEIQALCPQVTSMDQ 313
DB 330 LLYGSLNPPVPAVPAVKKMEDVAAOPORLDTADPAMLYAVDGVPTRMKEFRLLGLSE 389
OY 314 LPSRALGPAAAT-LSP-ESPAGSPMMIOPG-PQ-LYDVMADVPAARMKEFRTGLRE 369
DB 390 HIEERLEONGRCLEAHYSMLEAMRRTPRHEATLDVYGRVCDMNLRCLEINIRETLE 449
OY 370 ATEAVEVEIGR-FRDQOYEMLRKMRQOP--AGLGAVYALERGLDGCVEDLRSLQ 425

RESULT 6
ID FASA_PIG STANDARD: PRT: 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Expression of apoptosis-associated genes in hibernating and stunned
myocardium of pig.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DB EMBL: AJ001203; CA04596.1; -
DR PFAM: PF000020; TNFR_c6; 3.
DR HSSP: P25445; 1DDF.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 332
FT DOMAIN 17 175 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 176 192 POTENTIAL.
FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 164 3 X TNFR-CYS.
FT REPEAT 45 81 TNFR-CYS 1.
FT REPEAT 82 125 TNFR-CYS 2.
FT REPEAT 126 164 TNFR-CYS 3.
FT DOMAIN 227 311 DEATH DOMAIN.

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FT CARBOHYD 38 38
FT CARBOHYD 116 116
SQ SEQUENCE 332 AA; 37592 MM; 5B8B03662756BFB1B CRC64;
Query Match 8.5%; Score 278; DB 1; Length 332;
Best Local Similarity 38.2%; Pred. No. 2,14e-34;
Matches 42; Conservative 21; Mismatches 38; Indels 9; Gaps 7;

DB 45 ECPGQHRE-GQFCQCPQPCRRKHADCTSPGAPQCPGSEGEYTD-KNHSSKCRRC 102
OY 45 DCAQDFHKKIKGLFCCRCRPAHYLKAPCTEPCGNSCTLCVPO-DYFLAMENHNSECARC 103
DB 103 RVCGEGHLEVE-KNCTRTONTKCRCKRNF--CHTSQCEHCNP--CTTC 147
OY 104 QACD-EQASQVALPNCASVADTRCGCRGMYECQVSQVSSPFCYOPC 152

RESULT 7
ID FASA_BOVIN STANDARD: PRT: 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 96226401.
RA too J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234(1996).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC -----
DB EMBL: U34794; AAC48546.1; -
DR HSSP: P25445; 1DDF.
DR PFAM: PF000020; TNFR_c6; 3.
DR PFAM: PF00531; death; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 323
FT DOMAIN 17 170 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 171 188 POTENTIAL.
FT DOMAIN 189 323 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 45 163 3 X TNFR-CYS.
FT REPEAT 45 80 TNFR-CYS 1.

```



FT	REPEAT	81	124	TNFR-CYS 2.
FT	REPEAT	125	163	TNFR-CYS 3.
FT	DOMAIN	238	306	DEATH DOMAIN.
SQ	SEQUENCE	323 AA:	36445 MW;	4D8B8A90E9E1F4892 CRC64;
Query Match		6.5%;	Score 213;	DB 1; Length 323;
Best Local Similarity		29.5%;	Pred. No. 5.49e-21;	
Matches	31; Conservative	24;	Mismatches 43;	Indels 7; Gaps 5;
Dd	55	FCCGCPPEKRRKNDCCKRDGTPECVLCSSEGETYD-KSHSDKCIRSCIDDERGLEVE	113	
Oy	57	FCRCRCPAGHYLKACETPCGNSCTLPQO-DTFAMENHNHSECARQACDEASOVAL	115	
Bb	114	ONCTRNTAKCRCKSNFN--CNSSPCEHCNP--CPTC-EHGIIER	153	
Oy	116	EMCSAVADTRCCCKRGWIECYQSVCVSSPRYCQPCIDCGALHR	160	
RESULT	8	STANDARD:	PRT;	324 AA.
ID	FASA_RAT			
AC	063199;			
Df	15-JUL-1999 (Rel. 38, Created)			
Df	15-JUL-1999 (Rel. 38, Last sequence update)			
Df	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	FAST RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS) (APO-1 ANTIGEN) (CD95).			
GN	AP1 OR FAS.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;			
RX	MEDLINE: 94128114.			
RA	Kimura K., Yamamoto M., Wakatsuki T.;			
RT	"A variant mRNA species encoding a truncated form of Fas antigen in the rat liver."			
RL	Biochem. Biophys. Res. Commun. 198:666-674(1994).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE. IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T-CELLS, OR BORN (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.			
CC	-1- SIMILARITY: CONTAINS A LA-NGRF/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	-----			
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CC	-----			
DR	EMBL, D26112; BAA05108.1; -			
DR	PFAM, PF00020; TNFR.c6; 3.			
DR	PFAM, PFO0531; death; 1.			
DR	PROSITE, PS00652; TNFR_NGFR_1; 2.			
DR	PROSITE, PS50050; TNFR_NGFR_2; 1.			
DR	PROSITE, PS50017; DEATH_DOMAIN.1.			
KW	Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; signal.			
FT	SIGNAL	1	21	BY SIMILARITY.
FT	CHAIN	22	324	FASL RECEPTOR.
FT	DOMAIN	22	171	INTRACELLULAR (POTENTIAL).
FT	TRANSMEM	172	168	POTENTIAL.
FT	DOMAIN	189	324	CYTOPLASMIC (POTENTIAL). 3 X TNFR-CYS.
FT	DOMAIN	43	163	

FT	REPEAT	43	79	TNFR-CYS 1.
FT	REPEAT	80	123	TNFR-CYS 2.
FT	REPEAT	124	163	TNFR-CYS 3.
FT	DOMAIN	219	303	DEATH DOMAIN.
FT	CARBOHYD	43	43	POTENTIAL.
FT	CARBOHYD	114	114	POTENTIAL.
FT	CARBOHYD	132	132	POTENTIAL.
SO	SEQUENCE	324 AA;	36835 MM;	D25D583C909D9D09 CRC64;

Query Match	6.5%;	Score 211;	DB 1;	Length 324;
Best Local Similarity 30.1%;		Pred. No. 1.37e-20;		
Matches 37;	Conservative	26;	Mismatches 47;	Indels 13; Gaps 12.

Db	43	NCSEELXO-VSPFCOPCPQGERVKVD-CTTSGGAPTCPCTEGEEXTDR-KHYSDCRR	99
OY	45	DOAGDFHKKIGLFCRCGPAG-HYLKAPCTPCGNSCTGLVCPQ-DTEFLAMHHNSCAR	102
Db	100	CAFCDGEGLEVE-TNCRONTGCRCKENY--CNSLCC-DHC-YNCTSGGLE-DLLEP	153
OY	103	COACCE-OASQVALENCASVADTRGCKPQWFEQVQSQCVSSTSPFYCPQC-LDGCALHR	160
Db	154	CTR	156
OY	161	HTR	163

RESULT	9	STANDARD;	PRT;	327 AA.
AC	P25446;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-MAY-1997 (Rel. 35, Last annotation update)			
DE	FAST RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)			
DE	(APO-1 ANTIGEN) (CD95).			
GN	AP1 OR FAS.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RX	SEQUENCE FROM N.A.			
RX	MEDLINE: 92148151.			
RA	Watanabe-Fukunaga R., Brannan C.I., Itoh N., Yonehara S.,			
RA	Copeland N.G., Jenkins N.A., Nagata S.;			
RT	"The cDNA structure, expression, and chromosomal assignment of the			
RT	mouse Fas antigen."			
RL	J. Immunol. 148:1274-1279(1992).			
RN	[2]			
RN	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE: 93189576.			
RX	Adachi M., Watanabe-Fukunaga R., Nagata S.;			
RT	"Aberrant transcription caused by the insertion of an early			
RT	transposable element in an intron of the Fas antigen gene of 1pr			
RT	mouse."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:1756-1760(1993).			
RL	[3]			
RN	VARIANT LPR.			
RX	MEDLINE: 92195401.			
RA	Watanabe-Fukunaga R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Nagata S.;			
RT	"Lymphoproliferation disorder in mice explained by defects in Fas			
RT	antigen that mediates apoptosis."			
RL	Nature 356:314-317(1992).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE			
CC	ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED			
CC	RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING			
CC	SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC			
CC	ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF			
CC	CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING			
CC	APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE			
CC	INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED			
CC	SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- TISSUE SPECIFICITY: DETECTED IN VARIOUS TISSUES INCLUDING THYMUS,			



CC LIVER, LUNG, HEART, AND ADULT OVARY.  
 CC - DOMAIN CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC - DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION  
 CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY  
 CC PRODUCTION.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC -----  
 DR EMBL: M83649; AAA37593.1; -  
 DR EMBL: S56490; AAB25700.1; -  
 DR EMBL: S56485; AAB25700.1; JOINED.  
 DR EMBL: S56486; AAB25700.1; JOINED.  
 DR PIR: A46484; A46484.  
 DR HSP: P25445; 1DDF.  
 DR MGD: MGI:95484; FAS.  
 DR PFAM: PF00020; TNFR\_c6; 3.  
 DR PFAM: PF00531; death; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
 DR PROSITE: PS00505; TNFR\_NGFR.2; 2.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.1.  
 DR Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
 KM Disease mutation.  
 FT SIGNAL 1 21  
 FT CHAIN 22 327 FASL RECEPTOR.  
 FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 170 186 POTENTIAL.  
 FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 43 162 3 X TNFR-CYS.  
 FT REPEAT 43 79 TNFR-CYS 1.  
 FT REPEAT 80 123 TNFR-CYS 2.  
 FT REPEAT 124 162 TNFR-CYS 3.  
 FT DOMAIN 222 306 DEATH DOMAIN.  
 FT CARBOHYD 43 43 POTENTIAL.  
 FT CARBOHYD 114 114 POTENTIAL.  
 FT VARIANT 246 246 I -> N (IN LPR).  
 SQ SEQUENCE 327 AA; 37418 MW; F6BFC5ACE356EE CRC64;

Query Match 6.28; Score 204; DB 1; Length 327;  
 Best Local Similarity 27.9%; Pred. No. 3.32e-19;  
 Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;

DB 43 NCSEGLYOC-GPCCGPOCPGKKKVVDCMKNGTPTCAPCTEGKEKEMD-KNHYADKRCR 100  
 QY 45 DAGDFHKKITGLFCRCGCGPAGHLYLKPCPEPCGNSRLVCPPDT-FLAMENHNHNSCARC 103  
 DB 101 TLCDERHGLEVEFNCTLTONTCKCKKPDYCDSPGCEHCYRCAS 144  
 QY 104 QACDEGASQVALENCASAVADTRCGCKPGMVEQYVS-QCVSSSP 146

RESULT 10  
 ID FASL\_HUMAN STANDARD: PRT; 335 AA.  
 AC P25445;  
 DT 01-MAY-1992 (Rel. 22, Last Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
 DE (APO-1 ANTIGEN) (CD95 ANTIGEN).  
 GN APT1 OR FAS.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91309137.

RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,  
 RA Sameshima M., Hase A., Seto Y., Nagata S.;  
 RT "The polypeptide encoded by the cDNA for human cell surface antigen  
 RT Fas can mediate apoptosis.";  
 RL Cell 66:233-243(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.  
 RX MEDLINE: 92268122.  
 RA Oehm A., Behrmann I., Falk W., Pawlita M., Maier G., Klas C.,  
 RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponsingl H.,  
 RA Krammer P.H.;  
 RT "Purification and molecular cloning of the Apo-1 cell surface  
 RT antigen, a member of the tumor necrosis factor/neve growth factor  
 RT receptor superfamily. Sequence identity with the Fas antigen.";  
 RL J Biol. Chem. 267:10709-10715(1992).  
 RN [3]  
 RP STRUCTURE BY NMR OF 218-335.  
 RX MEDLINE: 97122332.  
 RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;  
 RT "NMR structure and mutagenesis of the Fas (Apo-1/CD95) death domain.";  
 RL Nature 384:638-641(1996).  
 CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
 CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH.  
 CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC - DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
 CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC - DATABASE: NAME=PROW; NOTE=CD guide CD95 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd95.htm".  
 CC -----  
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 CC -----  
 DR EMBL: M67454; AAA63174.1; -  
 DR EMBL: X63717; CAA45250.1; -  
 DR PIR: A40036; A40036.  
 DR PIR: S24543; S24543.  
 DR PDB: 1DDF; 12-NOV-97.  
 DR MIM: 134637; -  
 DR PFAM: PF00020; TNFR\_c6; 2.  
 DR PFAM: PF00531; death; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
 DR PROSITE: PS00505; TNFR\_NGFR.2; 2.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.1.  
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
 KM 3D-structure.  
 FT SIGNAL 1 16  
 FT CHAIN 17 335 FASL RECEPTOR.  
 FT DOMAIN 17 173 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 174 190 POTENTIAL.  
 FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 47 166 3 X TNFR-CYS.  
 FT REPEAT 47 83 TNFR-CYS 1.  
 FT REPEAT 84 127 TNFR-CYS 2.  
 FT REPEAT 128 166 TNFR-CYS 3.  
 FT DOMAIN 230 314 DEATH DOMAIN.  
 FT CARBOHYD 118 118 POTENTIAL.  
 FT CARBOHYD 136 136 POTENTIAL.  
 SQ SEQUENCE 335 AA; 37732 MW; 0139942535111410 CRC64;

Query Match 5.8%; Score 190; DB 1; Length 335;



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RM [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MONOCYTES:
RX MEDLINE: 92013149.
RA Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
RT "The T cell activation antigen CD27 is a member of the nerve growth
RL factor/tumor necrosis factor receptor gene family.";
RN J. Immunol. 147:3165-3169(1991).
RM [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93094588.
RA Loenen W.A., Gravestien L.A., Beumer S., Melief C.J., Hagemeijer A.,
RT Borst J.;
RT "Genomic organization and chromosomal localization of the human CD27
RL gene.";
RL J. Immunol. 149:3937-3943(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
CC A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.
CC -1- PTM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD27 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd27.htm".
CC -----
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CC -----
DR EMBL: M63928; AAA58411.1; -.
DR PIR: A46454; A46454.
DR PIR: A46517; A46517.
DR HSSP: P19438; INCF.
DR MIM: 186711; -.
DR PFAM: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR KW T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 260 CD27L RECEPTOR.
FT DOMAIN 21 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 212 POTENTIAL.
FT DOMAIN 213 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 141 3 X TNFR-CYS.
FT REPEAT 26 63 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 POTENTIAL.
FT MOD RES 219 219 PHOSPHORYLATION (POTENTIAL).
FT COMPLOC 59 59 A -> T (TN REF. 2)
SO SEQUENCE 260 AA; 29156 MW; 43C38B92FA90DE2 CRC64;

Query Match 5.4%; Score 177; DB 1; Length 260;
Best Local Similarity 25.2%; Pred. No. 5.28e-14;
Matches 32; Conservative 36; Mismatches 50; Indels 9; Gaps 7;

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RESULT 14
ID OX40_RAT STANDARD; PRT; 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).
GN TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-T-CELL;
RX MEDLINE: 90214614.
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
RL lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBL J. 9:1063-1068(1990).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL: X17037; CAA34897.1; -.
DR PIR: S08036; S08036.
DR PIR: S12783; S12783.
DR HSSP: P25942; ICDF.
DR PFAM: PF00020; TNFR_C6; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 271 OX40L RECEPTOR.
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 164 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 POTENTIAL.
SO SEQUENCE 271 AA; 29895 MW; C06465136B1E821 CRC64;

Query Match 5.1%; Score 165; DB 1; Length 271;
Best Local Similarity 29.7%; Pred. No. 8.94e-12;
Matches 22; Conservative 17; Mismatches 32; Indels 3; Gaps 3;

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Job time : 18 secs.

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
GN TXGP1 OR OX40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RX MEDLINE; 94044750.
RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
RA Claassen E., Noelle R.J., Fell H.;
RT "Cloning of mouse OX40: a T cell activation marker that may mediate
RT T-B cell interactions."
RL J. Immunol. 151:5261-5271(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95255413.
RA Birkehead M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
RA Barclay A.N.;
RT "Gene structure and chromosomal localization of the mouse homologue
RT of rat OX40 protein."
RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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-----
DR EMBL; Z21674; CAA79772.1; -
DR EMBL; X85214; CAA59476.1; -
DR HSSP; P25942; ICDF.
DR MGD; MG1:104512; TXGP1.
DR PFAM; PF00020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 2.
DR Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT 1 19 POTENTIAL.
FT CHAIN 20 272 OX40L RECEPTOR.
FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236 POTENTIAL.
FT DOMAIN 237 272 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 165 4 X TNFR-CYS.
FT REPEAT 26 61 TNFR-CYS 1.
FT REPEAT 62 103 TNFR-CYS 2.
FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 125 165 TNFR-CYS 4.
FT CARBOHYD 144 144 POTENTIAL.
FT CONFLICT 15 15 A->G (IN REF. 2).
SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;

Query Match 5.1%; Score 167; DB 1; Length 272;
Best local Similarity 30.0%; Pred. No. 3,84e-12;
Matches 33; Conservative 22; Mismatches 49; Indels 6; Gaps 6;

DB 5 VQOPTALLLL-ALTLYGT-ARRLNCVKHTYPS-GHKCCRCQPGHGMVSRCDHTROTLC 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 22 VPOALLLVLLGARAGGTGRPCDAGDFHKRIIGLFCRCGCPAGHYLPACTEPCGNSTC 81
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

DB 61 HPC-ETGEFVN-EAVNYDTCKQCTQCNHRSGSELKONCTPTQDTVCRCPRG 108
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 82 LVCPODTFLAMENHHNSECARCQACDEQASQVALENCASAVADTRCGCKRG 131
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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Search completed: Tue Jul 25 22:20:18 2000

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MSrch\_PP protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Jul 25 22:22:48 2000; MasPar time 14.90 Seconds  
 Tabular output not generated. 867,424 Million cell updates/sec

Title: >US-09-314-889-4  
 Description: (1-417) from US09314889.pep  
 Perfect Score: 3198  
 Sequence: 1 MEQRPRGCANVAALLLVLL.....ERMIGDGVEDLRSLQKGP 417

Scoring table: PAM 150  
 Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: swiss-prot38  
 1:swissprot

Statistics: Mean 48.727; Variance 83.543; scale 0.583

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	ID	Description	Pred. No.
1	3198	100.0	417	1	WSL1_HUMAN WSL-1 PROTEIN PRECURSOR	0.00e+00
2	407	12.7	455	1	TNR1_HUMAN TUMOR NECROSIS FACTOR	2.42e-62
3	399	12.5	454	1	TNR1_MOUSE TUMOR NECROSIS FACTOR	1.49e-60
4	398	12.4	461	1	TNR1_PIG TUMOR NECROSIS FACTOR	2.50e-60
5	383	12.0	461	1	TNR1_RAT TUMOR NECROSIS FACTOR	5.52e-57
6	278	8.7	332	1	FASA_PIG FAST RECEPTOR PRECURSOR	3.52e-34
7	213	6.7	323	1	FASA_BOVIN FAST RECEPTOR PRECURSOR	7.37e-21
8	211	6.6	324	1	FASA_RAT FAST RECEPTOR PRECURSOR	1.83e-20
9	204	6.4	327	1	FASA_MOUSE FAST RECEPTOR PRECURSOR	4.35e-19
10	190	5.9	335	1	FASA_HUMAN FAST RECEPTOR PRECURSOR	2.22e-16
11	182	5.7	336	1	VT2_MYXL TUMOR NECROSIS FACTOR	7.37e-15
12	179	5.6	349	1	VC22_VARH PROTEIN C2/28 HOMOLOG	2.70e-14
13	174	5.4	260	1	CD27_HUMAN CD27L RECEPTOR PRECURS	2.32e-13
14	168	5.3	461	1	TNR2_HUMAN TUMOR NECROSIS FACTOR	2.97e-12
15	165	5.2	271	1	OX40_RAT TUMOR NECROSIS FACTOR	1.05e-11
16	164	5.1	325	1	OX40_SFVA TUMOR NECROSIS FACTOR	8.45e-11
17	160	5.0	272	1	OX40_MOUSE OX40L RECEPTOR PRECURS	1.28e-10
18	159	5.0	277	1	CD40_HUMAN CD40L RECEPTOR PRECURS	8.45e-11
19	160	5.0	435	1	TNR2_HUMAN TUMOR NECROSIS FACTOR	8.45e-11
20	161	5.0	474	1	TNR2_MOUSE TUMOR NECROSIS FACTOR	5.58e-11
21	157	4.9	250	1	CD27_MOUSE CD27L RECEPTOR PRECURS	2.91e-10
22	157	4.9	415	1	TNR2_MOUSE TUMOR NECROSIS FACTOR	2.91e-10
23	153	4.8	656	1	RIP_MOUSE SERINE/THREONINE PROTE	1.50e-09

24	146	4.6	416	1	NGFR_CHICK LOW-AFFINITY NERVE GRO	2.51e-08
25	139	4.3	427	1	NGFR_HUMAN LOW-AFFINITY NERVE GRO	3.96e-07
26	134	4.2	671	1	RIP_HUMAN SERINE/THREONINE PROTE	2.73e-06
27	131	4.1	425	1	NGFR_RAT LOW-AFFINITY NERVE GRO	8.53e-06
28	124	3.9	3635	1	LMA5_MOUSE LAMININ ALPHA-5 CHAIN	1.16e-04
29	114	3.6	277	1	OX40_HUMAN OX40L RECEPTOR PRECURS	4.14e-03
30	116	3.6	799	1	ITB5_HUMAN INTERFERIN BETA-5 PRECUR	2.06e-03
31	114	3.6	1247	1	NIDO_HUMAN NIDOGEN PRECURSOR (ENT	4.14e-03
32	111	3.5	655	1	ITB5_PAPCT INTERFERIN BETA-5 (FRAG	1.17e-02
33	111	3.5	1607	1	LMG1_MOUSE LAMININ GAMMA-1 CHAIN	1.17e-02
34	112	3.5	1609	1	LMG1_HUMAN LAMININ GAMMA-1 CHAIN	8.28e-03
35	108	3.4	103	1	VA53_VACCV PROTEIN A53.	3.23e-02
36	108	3.4	103	1	VA53_VACCV PROTEIN A53.	3.23e-02
37	110	3.4	269	1	CD40_BOVIN CD40L RECEPTOR PRECURS	1.64e-02
38	110	3.4	289	1	CD40_MOUSE CD40L RECEPTOR PRECURS	1.64e-02
39	109	3.4	400	1	LMB_HIRME LAMININ B-CHAIN (FRAG	2.31e-02
40	108	3.4	612	1	OCTC_RAT PEROXISOMAL CARBONINE	3.23e-02
41	108	3.4	647	1	GAG_SFVL GAG POLYPROTEIN (CORE	3.23e-02
42	108	3.4	1245	1	NIDO_MOUSE NIDOGEN PRECURSOR (ENT	3.23e-02
43	109	3.4	1789	1	LMR1_MOUSE LAMININ BETA-1 CHAIN P	2.31e-02
44	109	3.4	3707	1	PCBM_MOUSE BASEMENT MEMBRANE-SPEC	2.31e-02
45	107	3.3	883	1	PCGB_MOUSE BREVICAN CORE PROTEIN	4.51e-02

## ALIGNMENTS

RESULT 1 STANDARD; PRT; 417 AA.  
 ID WSL1\_HUMAN AC 093038; Q93036; Q93037; Q92983; P78515; Q99831; Q99722; P78507;  
 AC 099830;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-FEB-2000 (Rel. 39, Last annotation update)  
 DE WSL-1 PROTEIN PRECURSOR (APOPTOSIS-MEDIATING RECEPTOR DR3) (APOPTOSIS-  
 MEDIATING RECEPTOR TRAMP) (DEATH DOMAIN RECEPTOR 3) (WSL PROTEIN)  
 DE (APOPTOSIS INDUCING RECEPTOR AIR) (APO-3) (LYMPHOCYTE ASSOCIATED  
 DE RECEPTOR OF DEATH) (LARD).  
 GN TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND MUTAGENESIS.  
 RC TISSUE-LYMPHOID.  
 RX MEDLINE; 97088617.  
 RA Kitzman J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T.,  
 RA Grinham C.J., Brown R., Farrow S.N.;  
 RT "A death-domain-containing receptor that mediates apoptosis.";  
 RL Nature 384:372-375(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-UMBILICAL VEIN ENDOTHELIAL CELLS;  
 RX MEDLINE; 97081063.  
 RA Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M.,  
 RA Dunn D.R., Xing L., Gentz R., Ni J., Dixit V.M.;  
 RT "Signal transduction by DR3, a death domain-containing receptor  
 related to TNFR-1 and CD95.";  
 RL Science 274:990-992(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G.;  
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-HEART;  
 RX MEDLINE; 97148200.  
 RA Marsters S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,  
 RA Goddard A.D., Bauer K.D., Ashkenazi A.;  
 RT "Apo-3, a new member of the tumor necrosis factor receptor family,  
 contains a death domain and activates apoptosis and NF-kappa-B.";  
 RL Curr. Biol. 6:1669-1676(1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.



OC Eumariota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;  
 RC Mammalia: Eutheria: Primates: Catarrhini: Homiinae: Homo.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=PLACENTA;  
 RA MEDLINE: 90235285.  
 RT Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W.,  
 RN Getanaga T., Granger G.A., Lentz R., Raab H., Kohn W.J., Goeddel D.V.,  
 RP "Molecular cloning and expression of a receptor for human tumor  
 RX necrosis factor.";  
 RA Cell 61:361-370(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 90235284.  
 RA Loetscher H., Pan Y.-C.E., Lahn H.-W., Gentz R., Brockhaus M.,  
 RN Tabuchi H., Lesslauer W.;  
 RP "Molecular cloning and expression of the human 55 kd tumor necrosis  
 RX factor receptor.";  
 RA Cell 61:351-359(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
 RX MEDLINE: 91006021.  
 RA Nophar Y., Kemper O., Brakebusch C., Engelmann H., Zwarg R.,  
 RN Aderka D., Holtmann H., Wallach D.;  
 RP "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA  
 RX for the type I TNF-R, cloned using amino acid sequence data of its  
 RT soluble form, encodes both the cell surface and a soluble form of the  
 RN receptor.";  
 RP EMBO J. 9:3269-3278(1990).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91090841.  
 RA Himmler A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 RN Lantz M., Olsson I., Houghman R., Stratowa C., Adolf G.R.;  
 RP "Molecular cloning and expression of human and rat tumor necrosis  
 RX factor receptor chain (p60) and its soluble derivative, tumor  
 RN necrosis factor-binding protein.";  
 RP DNA Cell Biol. 9:705-715(1990).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=PLACENTA;  
 RA MEDLINE: 91017509.  
 RT Gray P.W., Barrett K., Chantry D., Turner M., Feldman M.;  
 RN "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
 RP expression of recombinant soluble TNF-binding protein.";  
 RX Proc. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 92250049.  
 RA Fuchs P., Strehl S., Dworzak M., Himmler A., Ambros P.F.;  
 RN "Structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
 RP localization to chromosome 12p13.";  
 RX Genomics 13:219-224(1992).  
 RN [7]  
 RP SEQUENCE OF 41-45.  
 RX MEDLINE: 90110215.  
 RA Engelmann H., Novick D., Wallach D.;  
 RN "Two tumor necrosis factor-binding proteins purified from human  
 RP urine. Evidence for immunological cross-reactivity with cell surface  
 RX tumor necrosis factor receptors.";  
 RA J. Biol. Chem. 265:151-1536(1990).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211.  
 RX MEDLINE: 93258809.  
 RA Banner D.W., D'Arcy A., Janes W., Gentz R., Schoenfeld H.-J.,  
 RN Broger C., Loetscher H., Lesslauer W.;  
 RP "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
 RX beta complex: implications for TNF receptor activation.";  
 RA Cell 73:431-445(1993).  
 RN [9]  
 RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
 RX MEDLINE: 97094982.  
 RA Natsumith J.H., Devine T.O., Khono H., Sprang S.R.;

RT	Structure of the extracellular domain of the type I tumor necrosis factor receptor. <sup>1</sup>	RT	Structure of the extracellular domain of the type I tumor necrosis factor receptor. <sup>1</sup>
RT	Structure 4:1251-1262(1996).	RT	Structure 4:1251-1262(1996).
RL	-1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR, THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS. CONTRIBUTES TO THE INDUCTION OF NONCYCLOCAL TNF EFFECTS INCLUDING ANTI-VIRAL STATE AND ACTIVATION OF THE ACID SPHINGOMYELINASE.	RL	-1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
CC	-1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.	CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC	-1- SIMILIARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.	CC	-1- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO THE DEATH DOMAIN. THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.
CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm"	CC	-1- SIMILIARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC	-----	CC	-1- DATABASE: NAME=PROV; NOTE=CD guide CD120a entry; WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120a.htm"
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@sib.ch">license@sib.ch</a> ).	CC	-----
CC	EMBL; X55313; CAA39021.1; -	CC	EMBL; X55313; CAA39021.1; -
DR	EMBL; M33294; AAA03210.1; -	DR	EMBL; M33294; AAA03210.1; -
DR	EMBL; M58286; AAA36753.1; -	DR	EMBL; M58286; AAA36753.1; -
DR	EMBL; M63121; AAA36754.1; -	DR	EMBL; M63121; AAA36754.1; -
DR	EMBL; M75866; AAA61201.1; -	DR	EMBL; M75866; AAA61201.1; -
DR	EMBL; M75865; AAA61201.1; JOINED.	DR	EMBL; M75865; AAA61201.1; JOINED.
DR	EMBL; M60275; AAA36756.1; -	DR	EMBL; M60275; AAA36756.1; -
DR	EMBL; A21522; CAA01558.1; -	DR	EMBL; A21522; CAA01558.1; -
DR	PIR; A34899; GQHDT1.	DR	PIR; A34899; GQHDT1.
DR	PIR; A35010; A35010.	DR	PIR; A35010; A35010.
DR	PIR; S12057; S12057.	DR	PIR; S12057; S12057.
DR	PIR; A38208; A38208.	DR	PIR; A38208; A38208.
DR	PDB; 1TNR; 3I-JUL-94.	DR	PDB; 1TNR; 3I-JUL-94.
DR	PDB; 1NCF; 07-DEC-95.	DR	PDB; 1NCF; 07-DEC-95.
DR	PDB; 1EXT; 11-JAN-97.	DR	PDB; 1EXT; 11-JAN-97.
DR	MM: 191190; -	DR	MM: 191190; -
DR	PFAM; PF00020; TNFR_C6; 4.	DR	PFAM; PF00020; TNFR_C6; 4.
DR	PFAM; PF00531; death; 1.	DR	PFAM; PF00531; death; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.	DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DR	PROSITE; PS00505; TNFR_NGFR_2; 3.	DR	PROSITE; PS00505; TNFR_NGFR_2; 3.
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	DR	PROSITE; PS50017; DEATH_DOMAIN; 1.
KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis; 3D-structure.	KW	Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis; 3D-structure.
FT	SIGNAL 1 21	FT	SIGNAL 1 21
FT	CHAIN 22 455	FT	CHAIN 22 455
FT	CHAIN 41 291	FT	CHAIN 41 291
FT	DOMAIN 22 211	FT	DOMAIN 22 211
FT	TRANSSEM 212 234	FT	TRANSSEM 212 234
FT	DOMAIN 235 455	FT	DOMAIN 235 455
FT	DOMAIN 43 196	FT	DOMAIN 43 196
FT	REPEAT 43 82	FT	REPEAT 43 82
FT	REPEAT 83 125	FT	REPEAT 83 125
FT	REPEAT 126 166	FT	REPEAT 126 166
FT	REPEAT 167 196	FT	REPEAT 167 196
FT	DOMAIN 338 348	FT	DOMAIN 338 348
FT	DOMAIN 356 441	FT	DOMAIN 356 441
FT	DISULFID 44 58	FT	DISULFID 44 58
FT	TUMOR NECROSIS FACTOR RECEPTOR 1.	FT	TUMOR NECROSIS FACTOR RECEPTOR 1.
FT	TUMOR NECROSIS FACTOR BINDING PROTEIN 1.	FT	TUMOR NECROSIS FACTOR BINDING PROTEIN 1.
FT	EXTRACELLULAR (POTENTIAL).	FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.	FT	POTENTIAL.
FT	CYTOLASMIC (POTENTIAL).	FT	CYTOLASMIC (POTENTIAL).
FT	4 X TNFR-CYS.	FT	4 X TNFR-CYS.
FT	TNFR-CYS 1.	FT	TNFR-CYS 1.
FT	TNFR-CYS 2.	FT	TNFR-CYS 2.
FT	TNFR-CYS 3.	FT	TNFR-CYS 3.
FT	TNFR-CYS 4.	FT	TNFR-CYS 4.
FT	N-SMASE ACTIVATION DOMAIN (NSD).	FT	N-SMASE ACTIVATION DOMAIN (NSD).
FT	DEATH DOMAIN.	FT	DEATH DOMAIN.

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FT DISULFID 59 72
FT DISULFID 62 81
FT DISULFID 84 99
FT DISULFID 102 117
FT DISULFID 105 125
FT DISULFID 127 143
FT DISULFID 146 158
FT DISULFID 149 166
FT DISULFID 168 179
FT DISULFID 182 191
FT DISULFID 185 195
FT CARBOHYD 54 54
FT CARBOHYD 145 145
FT CARBOHYD 151 151
FT CONFLICT 412 412
FT CONFLICT 443 446
FT CONFLICT 455 446
SQ SEQUENCE 455 AA; 50494 MM; 4CEFB96D03B8225 CMC64;

Query Match 12.7% Score 407; DB 1; Length 455;
Best Local Similarity 29.9%; Pred. No. 2,42e-62;
Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHIGDREKDSVPOCKYIHPONNSICCTKCHKGTLYLNCPPRGQDTCREES 86
19 LIGRAAGGTRSPR-CDCA-GDF-HKKTGLFCRCRCPAGHYLKAPCTEPGCGSTLVCPQ 75
87 GSFTASENHLE-RHLSGSKCRKEMGOVEISSCTVDRTFVCGCRKQRYHHY-SENILFC- 143
76 DTFLEAMENHNHSECARQADQASQVALLENGSAVADTRCCGKPGWFEQVSCVSSSP 135
144 FNCGLCLN-GIVH---LSCQKONTVC-TCHAGFLENECVSCSNCKSECTKLCIP 197
136 FYCPCPCDCGALHNRHLIC-SRRDTCGTCLPGFEHGDGCVSCPSTLIG-SCPERC-A 192
198 QIENWKTEDSGTIVLP-LYIFPGICLLSLFTGLMRYRQRMKSKLVSICGSKTPE 256
193 AVCGWRQMF-W-VQVLAGLVY--PL-LLGATLT-YTR-HCWPK--PLVTADBA-GME 242
257 GELEGTTRKPLAPNPFSPPTGFTTIGFSPVSTSTSTSTSTSTSTSTSTSTSTSTST 316
243 A-LTPRPATHLSPDS-AHTL-LAPRDSSEKICVQLVGN- WTPGYETQELCPQYT- 297
317 PYGADPILATLALSDPPLNPLQWEDSAHNPQSLDTPDPLTLYAVENVPPLMKFEVR 376
298 -W-SMDLPSPALCPAAPT-LSP-ESPAGSPAMLDOPG-LYDVMQAVARMRKKEVR 352
377 RLGSDEIDRLLELONGRCLEAREQSMATRRRRPREATTELLGRLMDMLGCLIED 436
353 TLGLREAEIENVEYGR-FRQOQTEMLKRWQOP--AGLGAVYALERRGLDGCYED 408
Db 437 IEEL 441
QY 409 LRSRL 413

RESULT 3
ID TNRI_MOUSE STANDARD; PRT; 454 AA.
AC P25118;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).
GN TNFRSF1A OR TNFR1 OR TNFR-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 9118785.
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species

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RT specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91246168.
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor";
RL Mol. Cell. Biol. 11:3020-3026(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91285014.
RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissenerghis A.M.,
RA Gray P.W., Feldmann M., Foxwell B.M.J.;
RT "Cloning, expression and cross-linking analysis of the murine p55
RT tumor necrosis factor receptor";
RL Eur. J. Immunol. 21:1649-1656(1991).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE-SPLEEN.
RN MEDLINE; 92039815.
RA Rotte J.G., Brockhaus M., Gentz R., Lesslauer W.;
RT "Molecular cloning and expression of the mouse Tnf receptor type b.";
RL Immunogenetics 34:338-340(1991).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94245292.
RA Bebo B.F., Linthicum D.S.;
RT "Nucleotide sequence of the TNF type I receptor from a mouse
RT endothelioma cell line.";
RL Immunogenetics 39:450-451(1994).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93156721.
RA Rothe J., Bluethmann H., Gentz R., Lesslauer W., Steimetz M.;
RT "Genomic organization and promoter function of the murine tumor
RT necrosis factor receptor beta gene.";
RL Mol. Immunol. 30:165-175(1993).
CC - FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD
CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING
CC AGGREGATE CAUDED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)
CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE
CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE
CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).
CC - SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO
CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS
CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY
CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING
CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO
CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX
CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND
CC NF-KAPPA B SIGNALING (BY SIMILARITY).
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL; M60468; AAA39751.1; -
DR EMBL; M59377; AAA40464.1; -
DR EMBL; X59238; CAA41922.1; -
DR EMBL; X57796; CAA40936.1; -
DR EMBL; L26349; AAA59361.1; -
DR EMBL; M76556; AAA40465.1; -
DR EMBL; M88067; AAA40465.1; JOINED.
DR EMBL; M76555; AAA40465.1; JOINED.
DR PIR; A38634; GOMST1.

```





FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 190 BY SIMILARITY.  
 FT DISULFID 185 194 BY SIMILARITY.  
 FT CARBOHYD 54 86 POTENTIAL.  
 FT CARBOHYD 86 86 POTENTIAL.  
 FT CARBOHYD 145 145 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 SQ SEQUENCE 461 AA; 50969 MW; CD72361EC60C9D43 CRC64;

Query Match 12.4%; Score 398; DB 1; Length 461;  
 Best Local Similarity 32.3%; Pred. No. 2.50e-60;  
 Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

DB 33 HPGRKRESICPOGKYSHPNRSICCTCKHKGTYLVSDSPSGQETVCVCDKGTFTAS 92  
 25 QGGRSRPR-CDCA-GDF-HKKIGLFCGCGPAGHILKAPCTEPGNSICVOPDFTFLAW 81  
 -DB 93 ENHL-TQCLSCSKCRSEMSQVEISPTVDRDTCGCRN--QYR-KY-WSETLF-Q-C 143  
 82 ENHNSCARCOACDEQASQVVALENCSSAVADTRCGCKPGMEVECVQSVSSSPYQPC 141  
 DB 144 LNC-SLCPNGVQVPLEKOPTICN-CHSGFPLRKBCVSCVNCNADCKNLCPTSTSR 201  
 142 LDCGALHHR-T-RLIC-SRDPDCTCLPGFYEHDGCVSCPTSLGSCPECAAVCGMR 198  
 DB 202 NDFDGTGTVLLPIVIFGLCLAFELFVGLACRYOR-WKPKLYSLICKSPVKEGDEEP 260  
 199 QMFV---VOVLLA-----GLVVPILLGATLVYTHRCWPHK--PLV-----TA-DAGMWA 243  
 DB 261 LAIAPSPGPTTSPDPSPTTSPVSPSPSSPTPTPCDSNINIVTSPKTIAPPP 320  
 244 L-TTP---PATHLSPDLS-AHTL-LAPDSSKICTVOLVGNSTWTP---GYPETOEALCP 294  
 DB 321 OGAGPILPMRPAHPVPRPLPKWGSASHSAPQAOLADADATYAYVDGVPFRWKEF 380  
 295 QVTWSMDLP-SRLGPPAAPTL--SPSPAGSPAMMLQPGQ-LYDWDVADPARWKEF 350  
 DB 381 VRRGLSEHETERLELONGRCLEAREQSMLEWRRTSRREATLELGLSGLVRLMDLGL 440  
 351 VRTGLRAELEAVEVELEGR-FRQGYEMLRWMO--QP-AGLGAVVAALERMGLDGV 406  
 DB 441 EDIEBAL-RGP 450  
 407 EDLRSRLRGCP 417

RESULT 5  
 ID TNRI-RAT STANDARD: PRT; 461 AA.  
 AC P22934;  
 DT 01-AUG-1991 (Rel. 19, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 15-JUN-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFRSF1A OR TNFR1 OR TNFR-1.  
 OS Rattus norvegicus (Rat).  
 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 91090841.  
 RA Hammar A., Maurer-Fogy I., Kroenke M., Scheurich P., Pfizenmaier K.,  
 RA Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
 RT "Molecular cloning and expression of human and rat tumor necrosis  
 RT factor receptor chain (p60) and its soluble derivative, tumor  
 RT necrosis factor-binding protein.";  
 RL DNA Cell Biol. 9:705-715(1990).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD  
 CC RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING  
 CC AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DISC)  
 CC PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE  
 CC SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE  
 CC PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO

CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 CC PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 CC TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 CC ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -----  
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 CC or send an email to [license@isb-slb.ch](mailto:license@isb-slb.ch)).  
 CC -----  
 CC EMBL; M63122; AAA42256.1; -;  
 DR PIR; B36555; B36555.  
 DR HSSP; P19438; 1TNF.  
 DR PFAM; PF00020; TNFR\_C6; 4.  
 DR PFAM; PF00531; death\_1; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Repeat; signal; Apoptosis.  
 FT CHAIN 1 21  
 FT SIGNAL 1 21  
 FT DOMAIN 22 461  
 FT TRANSMEM 22 211  
 FT DOMAIN 212 234  
 FT TRANSMEM 212 234  
 FT DOMAIN 235 461  
 FT DOMAIN 43 196  
 FT REPEAT 43 196  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT DOMAIN 344 354  
 FT DOMAIN 363 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 191  
 FT DISULFID 185 195  
 FT CARBOHYD 54 54  
 FT CARBOHYD 151 151  
 FT CARBOHYD 201 201  
 SQ SEQUENCE 461 AA; 50969 MW; EB23C05450FBD202 CRC64;

Query Match 12.0%; Score 383; DB 1; Length 461;  
 Best Local Similarity 29.8%; Pred. No. 5.52e-57;  
 Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;

DB 35 GDEKRDNLCPGQKYAHPRNNSICTCKHKGTYLVSDSPSGQETVCVCDKGTFTAS 94  
 27 GRSRPRCD-CA-GDF-HKKIGLFCGCGPAGHILKAPCTEPGNSICVOPDFTFLAW 83  
 DB 95 H-VROGLSKCTCKEMFQVEISPTKADMTVCGCKRKNQGRYISETHPCVDCSPFNGT 153  
 84 HNSRCARCOACDEQASQVVALENCSSAVADTRCGCKPGMEVECVQSVSSSPFYQ 139  
 DB 154 VTIIPCKE-KONTVNCNHAEPFLSGNCTPCSHCKNCKEOMKICLPYAVANTNPDSGTAV 212  
 140 PCLDGCALHHRRLILCSRDPTDGT-CLP-GFYEHDGCVS-C-PLSTIGSCPERCAAVC 195  
 DB 213 LPLVIFGLCLLFFICISILCRYPQWRPVYSIICRDSAPYKEVGEIGVTKPLTPASI 272

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OY 196 GNRQMWVQV-LLAGLVPL--LGATLVYR--CWRPKPLVADAG--EALTPPPA 249
DB 273 PAFSPNPGNPTLGSTTPRFSPVSTPISPVFGSNMHNPNVPAVEVPTQ-G-A-DP 329
OY 250 THLSPLD--AHTL-LAP-PPSSEKICTVOL--V-GNS-WTPGYPEQDCAICPQWTWMDQ 302
DB 330 LLYGSLNPVPIPAVRKMEVVAAPQRLDTPAPMLYAVVDGVPTRMKKEFMTLGLSE 389
OY 303 LBSRALGPAAPT-LSP-ESPAGSPAMLOPG-PQ-LYDMDAVPARKMEFVTLGLRE 358
DB 390 HIEERLELQNGRLREAHNSMLEAMRRTPRHEATLDVYGRVLCDMNLGLENIRETLE 449
OY 359 AELEAVEVEIGR-FRDOQYELMKRMHQGP---AGLCAVVAALERMGLDCCVEDLRSRLQ 414

RESULT 6
ID FASA_PIG STANDARD; PRT; 332 AA.
AC 07736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Sus. scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schultz R., Heusch G., Darmer D.;
RT *Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig.*;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC or send an email to license@sib-sib.ch).
CC
CC EMBL: AJ001202; CA04596.1; -.
CC PFAM: PF00020; TNFR_C6; 3.
CC
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS50050; TNFR_NGFR_2; 2.
CC PROSITE: PS50017; DEATH_DOMAIN; 1.
CC Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 16
CC CHAIN 17 332
CC DOMAIN 17 175
CC TRANSMEM 176 192
CC DOMAIN 193 332
CC DOMAIN 45 164
CC REPEAT 45 81
CC REPEAT 82 125
CC REPEAT 126 164
CC DOMAIN 227 311
CC DEATH DOMAIN.

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FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 116 116 POTENTIAL.
SQ SEQUENCE 332 AA; 37592 MW; 558B03682756BFLB CRC64;

Query Match
Best Local Similarity 38.2%; Pred. No. 3.52e-34;
Matches 42; Conservative 21; Mismatches 38; Indels 9; Gaps 7;

DB 45 ECPGQHRE-GQPCQPPPRKRRADCTSPGAGQCVPSCGEGLYTD-KNHSSKRCRC 102
OY 34 DCAQDFHRRKIGLFCRCRGPAGHYLKAAPTCEPGNTCLVCPQ-DYFLAMENHNSECAAC 92
DB 103 RVCGSEHLEVE-KNCTRTQNTKCRCKPNFF--CHTSQCEHNP--CTTC 147
OY 93 QACD-EQASQVALENCASVADTRCGCKRGWYECOVSSCVSSPYCQPC 141

RESULT 7
ID FASA_BOVIN STANDARD; PRT; 323 AA.
AC P51867;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN APT1 OR FAS.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE; 96226401.
RA yoo J., Stone R.T., Beattie C.W.;
RT *Cloning and characterization of the bovine Fas.*;
RL DNA Cell Biol. 15:227-234(1996).
CC -I- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -I- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC
CC EMBL: U34794; AAC48546.1; -.
CC HSPD: P25445; IDDE.
CC PFAM: PF00020; TNFR_C6; 3.
CC PFAM: PF00531; death; 1.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS50050; TNFR_NGFR_2; 2.
CC PROSITE: PS50017; DEATH_DOMAIN; 1.
CC Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 16
CC CHAIN 17 323
CC DOMAIN 17 170
CC TRANSMEM 171 188
CC DOMAIN 189 323
CC DOMAIN 45 163
CC REPEAT 45 80
CC TNFR-CYS 1.

```



CC LIVER, LUNG, HEART, AND ADULT OVARY.  
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -1- DISEASE: DEFECTS IN FAS ARE THE CAUSE OF A LYMPHOPROLIFERATION  
CC DISORDER (LPR) RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY  
CC PRODUCTION.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC -----  
DR EMBL: M83649; AAA37593.1; -;  
DR EMBL: S56490; AAB25700.1; -;  
DR EMBL: S56485; AAB25700.1; JOINED.  
DR EMBL: S56486; AAB25700.1; JOINED.  
DR PIR: A46484; A46484.  
DR HSSP: P25445; IDDP.  
DR MGD: MGI:95484; FAS.  
DR PFAM: PF00020; TNFR\_C6; 3.  
DR PFAM: PF00531; death; 1.  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
DR PROSITE: PS00050; TNFR\_NGFR.2; 2.  
DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
KW Disease mutation.  
FT SIGNAL 1 21  
FT CHAIN 22 327 FASL RECEPTOR.  
FT DOMAIN 22 169 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 170 186 POTENTIAL.  
FT DOMAIN 187 327 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 43 162 3 X TNFR-CYS.  
FT REPEAT 43 79 TNFR-CYS 1.  
FT REPEAT 80 123 TNFR-CYS 2.  
FT REPEAT 124 162 TNFR-CYS 3.  
FT DOMAIN 222 306 DEATH DOMAIN.  
FT CARBOHYD 43 43 POTENTIAL.  
FT CARBOHYD 114 114 POTENTIAL.  
FT VARIANT 246 246 I -> N (IN LPR).  
SQ SEQUENCE 327 AA: 37418 MW: F6BFFC5ACE356DEE CRC64;  
  
Query Match 6.48: Score 204; DB 1; Length 327;  
Best Local Similarity 27.9%; Pred. No. 4.35e-19;  
Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;  
  
DB 43 NCSEGLYGG-GPRCCQPCQPKKKKVEDCKKNNGGTPPCAPCTEGKEHYMD-KNHVADKRCRC 100  
-OY 34 DCAAGDHKKIKGLFCRCPCGKHYLAKRTPRCNSTCLVCPDPT-FLAMENHNHSEARC 92  
DB 101 TLDEEHGLEVETNCTLTONTCKCKRPDFCDSPGCEHCYRCAS 144  
OY 93 QACDEQASQVALENCASVADTRCGCKPGMWVEQOVS-QCVSSSP 135  
  
RESULT 10  
ID FASA\_HUMAN STANDARD; PRT; 335 AA.  
AC P25445;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)  
DE (APO-1 ANTIGEN) (CD95 ANTIGEN).  
GN APT1 OR FAS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91309137.

RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,  
RA Saneshima M., Hase A., Seto Y., Nagata S.;  
RT "The polypeptide encoded by the cDNA for human cell surface antigen  
RT Fas can mediate apoptosis.";  
RL Cell 66:233-243(1991).  
RN [2]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 226-240; 269-291 AND 321-335.  
RX MEDLINE: 92268122.  
RA Oelam A., Behnmann I., Falk W., Pawlita M., Maier G., Klas C.,  
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponsltingl H.,  
RA Kramer P.H.;  
RT "Purification and molecular cloning of the APO-1 cell surface  
RT antigen, a member of the tumor necrosis factor/reverse growth factor  
RT receptor superfamily. Sequence identity with the Fas antigen.";  
RL J. Biol. Chem. 267:10709-10715(1992).  
RN [3]  
RX STRUCTURE BY NMR OF 218-335.  
RX MEDLINE: 97122332.  
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.W.;  
RT "NMR structure and mutagenesis of the Fas (APO-1/CD95) death domain.";  
RL Nature 384:638-641(1996).  
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE  
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED  
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING  
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC  
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF  
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING  
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE  
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
CC SUICIDE OF MATURE T-CELLS, OR BOTH.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,  
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC -1- DATABASE: NME-PROT; NOTE-CD guide CD95 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd95.htm".  
CC -----  
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CC -----  
DR EMBL: M67454; AAA63174.1; -;  
DR EMBL: X63717; CAA45250.1; -;  
DR PIR: A40036; A40036.  
DR PIR: S24543; S24543.  
DR PDB: 1DDP; 12-NOV-97.  
DR MIM: 134637; -;  
DR PFAM: PF00020; TNFR\_C6; 2.  
DR PFAM: PF00531; death; 1.  
DR PROSITE: PS00652; TNFR\_NGFR.1; 2.  
DR PROSITE: PS00050; TNFR\_NGFR.2; 2.  
DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;  
KW 3D-structure.  
FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 335 FASL RECEPTOR.  
FT DOMAIN 17 173 EXTRACELLULAR (POTENTIAL).  
FT TRANSEM 174 190 POTENTIAL.  
FT DOMAIN 191 335 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 47 166 3 X TNFR-CYS.  
FT REPEAT 47 166 TNFR-CYS 1.  
FT REPEAT 84 127 TNFR-CYS 2.  
FT REPEAT 128 166 TNFR-CYS 3.  
FT DOMAIN 230 314 DEATH DOMAIN.  
FT CARBOHYD 118 118 POTENTIAL.  
FT CARBOHYD 136 136 POTENTIAL.  
SQ SEQUENCE 335 AA: 37732 MW: 0139942535111410 CRC64;  
  
Query Match 5.9%; Score 190; DB 1; Length 335;

Best Local Similarity 34.1%; Pred. No. 2,22e-16;  
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

Db 56 GQFCHKPCPGE-RKARDCTVNGDEPPCPCQEGKEYTD-KAHFSSKRCRCLDEGGL 113  
QY 44 GLFCRCRCPAGHYLKAP-CTEPCGNSCLVCPDPT-FLAMENHNHNSCARCOACDE-QAS 100

Db 114 EVEL-NCTRONTCKRCKPNEFCNSTVCEHC 143  
QY 101 QVALENCASAVADTRCGCKPWFVECOVS-QC 130

RESULT 11  
ID VRT.MYXVL STANDARD; PRT; 326 AA.

AC P29825;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).  
GN T2.  
OS Myxoma virus (Strain Lausanne).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Leporipoxvirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 91335768.

RA Upton C., Macen J.L., Schreiber M., McFadden G.;  
RT "Myxoma virus expresses a secreted protein with homology to the tumor  
necrosis factor receptor gene family that contributes to viral  
virulence."  
RT virulence."  
RL virology 184:370-382(1991).  
CC -I- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO  
REACH CELLULAR TARGET AND THEREBY DEAMENING THE POTENTIAL  
ANTIVIRAL EFFECTS OF THE CYTOKINE.

CC -I- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
CC CC  
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CC EMBL: M95181; AAA46632.1; -;  
DR EMBL: A23729; CAA01688.1; -;  
DR PIR: A40566; GQVZML.

DR HSSP: P19438; TNFR.  
DR PFAM: PF00020; TNFR\_C6; 2.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS00652; TNFR\_NGFR\_2; 2.  
KW Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 16 POTENTIAL.  
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.  
FT DOMAIN 27 186 4 X TNFR-CYS.  
FT REPEAT 27 62 TNFR-CYS 1.  
FT REPEAT 63 104 TNFR-CYS 2.  
FT REPEAT 105 147 TNFR-CYS 3.  
FT REPEAT 148 186 TNFR-CYS 4.  
FT CARBOHYD 66 66 POTENTIAL.  
FT CARBOHYD 181 181 POTENTIAL.  
FT CARBOHYD 205 205 POTENTIAL.  
FT CARBOHYD 238 238 POTENTIAL.  
SQ SEQUENCE 326 AA; 35208 MW; ABBF027E947292FF CRC64;

Query Match 5.7%; Score 182; DB 1; Length 326;  
Best Local Similarity 30.9%; Pred. No. 7.37e-15;  
Matches 34; Conservative 23; Mismatches 45; Indels 8; Gaps 8;

Db 5 TLLAVACVGGGAGPYGADRCRGNDYERKDL-CCTCSPGPGYASRLCG-PGSPYVS 62  
QY 14 ALLVLVIGARAGGTR-SP-RCDCAGDFHKTGLFCRCRCPAGHYLKAPCTEPCGNSL 71

Db 63 PCKNETFTA-STNHAPACVSCRGRTGHLSE-S-OSCDTRDRVDCSSAG 109  
QY 72 VQPDFTFLAMENHNHNSCARCOA-CDEQASQVALENCASVADTRCGCKRG 120

RESULT 12  
ID VC22.VARV STANDARD; PRT; 349 AA.

AC P34015;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-JUN-1994 (Rel. 29, Last annotation update)  
DE PROTEIN C22/B28 HOMOLOG.  
GN G4R.

OS Variola virus.  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Orthopoxvirus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-INDIA-1967 / ISOLATE IND3;  
RX MEDLINE: 93202281.  
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;  
RT "Genes of variola and vaccinia viruses necessary to overcome the host  
protective mechanisms."  
RT FEMS Lett. 319:80-83(1993).  
CC -I- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.

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CC EMBL: X69198; CAA49137.1; -;  
DR EMBL: X67117; CAA47340.1; -;  
DR PIR: D36858; D36858.  
DR PIR: S35987; S35987.  
DR PIR: S46888; S46888.  
DR HSSP: P19438; TNFR.  
DR PFAM: PF00020; TNFR\_C6; 2.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS00652; TNFR\_NGFR\_2; 2.  
KW Repeat.

FT DOMAIN 31 108 2 X TNFR-CYS.  
FT REPEAT 31 66 TNFR-CYS 1.  
FT REPEAT 67 108 TNFR-CYS 2.  
SQ SEQUENCE 349 AA; 38189 MW; D45D40B5CCE780EF CRC64;

Query Match 5.6%; Score 179; DB 1; Length 349;  
Best Local Similarity 27.1%; Pred. No. 2.70e-14;  
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7;

Db 15 IINGDAAPIPPNCKKCDTEY-KRHN-CLLSCPRGYASLCL-DSKNTDCTCGGSS 71  
QY 18 VILGARAGGTRPRDCD-AGDFHKTGLFCRCRCPAGHYLKAPCTEPCGNSCLVCPD 76

Db 72 TFLSRNNHL-PACLSGNGRGN-SNOVETRSCNTTNRIECSPGY 115  
QY 77 TFLAMENHNHNSCARCOA-CDEQASQVALENCASVADTRCGCKPWF 122

RESULT 13  
ID CD27.HUMAN STANDARD; PRT; 260 AA.

AC P26842;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14).  
GN TNFRSF7 OR CD27.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MONOCYTES:
RX MEDLINE: 92013149.
RA Camerini D., Walz G., Loenen W.A.M., Borst J., Seed B.;
RT "The T cell activation antigen CD27 is a member of the nerve growth
RT factor/tumor necrosis factor receptor gene family.";
RL J. Immunol. 147:3165-3169(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93094588.
RA Loenen W.A., Gravestien L.A., Beumer S., Melief C.J., Hagemeijer A.,
RA Borst J.;
RT "Genomic organization and chromosomal localization of the human CD27
RT gene.";
RL J. Immunol. 149:3937-3943(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD27L. MAY PLAY
CC A ROLE IN SURVIVAL OF ACTIVATED T-CELLS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN MOST T LYMPHOCYTES.
CC -1- PTM: PHOSPHORYLATED AND O-GLYCOSYLATED (PROBABLE).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME-PROV; NOTE-CD guide CD27 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd27.htm".
CC -----
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CC -----
DR EMBL: M63928; AAA58411.1; -.
DR PIR: A46454; A46454.
DR PIR: A46517; A46517.
DR HSSP: P19438; INCF.
DR MIM: 186711; -.
DR PIR: P00020; TNFR_c6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
KW T-cell; Glycoprotein; Transmembrane; Signal; Receptor; Repeat;
KW Phosphorylation.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 260 CD27L RECEPTOR.
FT DOMAIN 21 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 212 POTENTIAL.
FT DOMAIN 213 260 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 141 3 X TNFR-CYS.
FT REPEAT 26 63 TNFR-CYS 1.
FT REPEAT 64 104 TNFR-CYS 2.
FT REPEAT 105 141 TNFR-CYS 3.
FT CARBOHYD 95 95 POTENTIAL.
FT MOD_RES 219 219 PHOSPHORYLATION (POTENTIAL).
FT CONFLICT 59 59 A -> T (IN REF. 2).
SO SEQUENCE 260 AA; 29156 MW; 43C8B92FA90DME2 CRC64;

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Query Match 5.48; Score 174; DB 1; Length 260;
Best Local Similarity 25.48; Pred. No. 2,32e-13;
Matches 31; Conservative 34; Mismatches 48; Indels 9; Gaps 7;

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DB 9 LCVLGLVIGSATPPAPR-SCPERHYMAQGLCCMCERPGTFLLVDCDQHRKAACDCPCIP 67
OY 17 LVLLGA-RAAGGTRSPDCDAGFHKRIGFCGCGCPAGHLKAPCEPCGNSSTLYC-P 74
DB 68 GVSFSP-DHTRPHCECRHCN--SGLL-VRNCTITANAECAKNGW--OCRDKECTCD 121
OY 75 QDFLFAMENHNHSCARCACQACDEQASOALENCASAVADTRCGCKPGRNFVECVSOVCYSSS 134
DB 122 PL 123
OY 135 PF 136

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RESULT 14
ID TNFR2_HUMAN STANDARD: PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
DE BINDING PROTEIN 2) (TNFR2) (P80) (TNF-R2) (P75) (CD120b) (ETANERCEPT).
DN TNFRSF1B OR TNFR2 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 90260639.
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.;
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91045991.
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96299745.
RA Bellingier C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepassier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE: 90349572.
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.;
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE: 90110215.
RA Engelmann H., Novick D., Wallach D.;
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 22-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE: 91036048.
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Broekhaus M.;
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE: 93016040.
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.;
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.

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RX MEDLINE: 99221490.  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACOLOGICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND  
 CC MYER-AERST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID  
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING  
 CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO  
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/CD/CD120b.htm".  
 CC -1- DATABASE: NAME-Enbrel; NOTE-clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
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 CC -----  
 DR EMBL: M33315; AAA59929.1; -;  
 DR EMBL: M35857; AAA63262.1; -;  
 DR EMBL: U52165; AAC50622.1; -;  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -;  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.  
 DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MIM: 191191; -;  
 DR PFAM: PF00020; TNFR\_C6; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 258 287 POTENTIAL.  
 FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 39 201 4 X TNFR-CYS.  
 FT REPEAT 39 76 TNFR-CYS 1.  
 FT REPEAT 77 118 TNFR-CYS 2.  
 FT REPEAT 119 162 TNFR-CYS 3.  
 FT REPEAT 163 201 TNFR-CYS 4.  
 FT DISULFID 40 53 BY SIMILARITY.  
 FT DISULFID 54 67 BY SIMILARITY.  
 FT DISULFID 57 75 BY SIMILARITY.  
 FT DISULFID 78 93 BY SIMILARITY.  
 FT DISULFID 96 110 BY SIMILARITY.  
 FT DISULFID 100 118 BY SIMILARITY.  
 FT DISULFID 120 126 BY SIMILARITY.  
 FT DISULFID 134 143 BY SIMILARITY.  
 FT DISULFID 137 161 BY SIMILARITY.

FT DISULFID 164 179 BY SIMILARITY.  
 FT CARBOHYD 171 171 POTENTIAL.  
 FT CARBOHYD 193 193 POTENTIAL.  
 FT CONFLICT 141 141 R -> P (IN REF. 4).  
 FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).  
 FT CONFLICT 363 363 A -> T (IN REF. 4).  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
 Query Match 5.3%; Score 168; DB 1; Length 461;  
 Best Local Similarity 27.6%; Pred No. 2,97e-12;  
 Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;  
 Db 44 EYDPTAQMCCSKSPGGHAYFCTKT SDTVCSCEDESTYTQIM-NW-VPECLSCGSRG 100  
 Qy 38 DEHKHIGLFCGCGPAGHYLKPCTPCGNSYCLVCPDFTFLA-WENHNHNSCARCOA-C 95  
 Db 101 S-SQVETQACTRQNRNCTCRPMY 125  
 Qy 96 DEQASVALENCNAVADTRCGCKPMWF 122  
 RESULT 15  
 ID OX40\_RAT STANDARD; PRT; 271 AA.  
 AC P15725;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN) (MRC OX40).  
 GN TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-CELL.  
 RX MEDLINE: 90214614.  
 RA Mallett S., Fossum S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T  
 RT lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMBO J. 9:1063-1068(1990).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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 CC -----  
 DR EMBL: X17037; CAA34897.1; -;  
 DR PIR: S08036; S08036.  
 DR PIR: S12783; S12783.  
 DR HSSE: P25942; ICDF.  
 DR PFAM: PF00020; TNFR\_C6; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 271 OX40L RECEPTOR.  
 FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 211 235 POTENTIAL.  
 FT TRANSMEM 236 271 POTENTIAL.  
 FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 164 4 X TNFR-CYS.  
 FT REPEAT 25 60 TNFR-CYS 1.  
 FT REPEAT 61 102 TNFR-CYS 2.  
 FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 124 164 TNFR-CYS 4.  
 FT CARBOHYD 143 143 POTENTIAL.





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Mparch\_dp protein - protein database search, using Smith-Waterman algorithm  
 Run on: Tue Jul 25 22:24:16 2000; Maspar time 23.31 seconds  
 Tabular output not generated. 843.833 Million cell updates/sec

Title: >US-09-314-889-4  
 Description: (1-417) from US09314889.pep  
 Perfect Score: 3198  
 Sequence: 1 MEQRRCAGAAVALLLVLL.....ERMGIDGCVEDLRSLQKGP 417

Scoring table:  
 PAM 150  
 Gap 11

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: p1r64  
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 47.731; Variance 92.974; scale 0.513

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	407	12.7	455	1	GOHUT1 tumor necrosis factor	7.65e-55
2	399	12.5	454	1	GOHUT1 tumor necrosis factor	2.92e-53
3	398	12.4	461	2	JC4302 tumor necrosis factor	4.61e-53
4	385	12.0	454	2	J57826 tumor necrosis factor	1.68e-50
5	383	12.0	461	1	GOHUT1 tumor necrosis factor	4.15e-50
6	211	6.6	324	2	JC2395 Fas antigen precursor	8.54e-18
7	204	6.4	327	2	A46484 apoptosis-mediating m	1.42e-16
8	190	5.9	314	2	J37383 Fas soluble protein	3.60e-14
9	190	5.9	335	2	A40036 apoptosis-mediating s	3.60e-14
10	182	5.7	326	1	GOV2ML T2 protein - myxoma v	8.07e-13
11	179	5.6	349	2	D36858 gene G4R protein - va	2.56e-12
12	174	5.4	260	1	A46517 CD27 antigen precursor	1.73e-11
13	168	5.3	461	1	A35356 tumor necrosis factor	1.67e-10
14	165	5.2	271	1	S12783 OX40 antigen precursor	5.14e-10
15	164	5.1	325	2	B43692 T2 protein - rabbit f	7.46e-10
16	160	5.0	272	2	A48700 gene OX40 protein - m	3.29e-09
17	159	5.0	277	2	A60771 B-cell activation pro	4.75e-09
18	160	5.0	435	2	A54182 tumor necrosis factor	3.29e-09
19	161	5.0	474	2	B38634 tumor necrosis factor	2.27e-09
20	157	4.9	250	1	A49053 CD27 antigen precursor	9.90e-09
21	157	4.9	250	1	A48854 gene murine tumour ne	9.90e-09
22	153	4.8	656	2	I49299 receptor interacting	4.25e-08
23	146	4.6	416	1	JN0006 nerve growth factor r	5.24e-07

24	139	4.3	427	1	GOHUN nerve growth factor r	6.14e-06
25	372	4.2	372	2	I38992 receptor interacting	3.44e-05
26	134	4.2	671	2	T09479 serine/threonine prot	3.44e-05
27	131	4.1	425	1	A26431 nerve growth factor r	9.34e-05
28	125	3.9	132	2	S57566 Fas/Apo-1/CD95 protei	7.07e-04
29	125	3.9	149	2	S58662 Fas-Delta-(4,7) prote	7.07e-04
30	124	3.9	1808	2	T15099 hypothetical protein	9.82e-04
31	124	3.9	3635	2	T10053 laminin alpha 5 chain	9.82e-04
32	121	3.8	1574	2	T13954 MEGF6 protein - rat	2.61e-03
33	117	3.7	407	2	C70816 hypothetical protein	9.42e-03
34	114	3.6	277	2	I37552 OX40 homolog - human	2.42e-02
35	116	3.6	799	2	A38308 integrin beta-5 chain	1.29e-02
36	114	3.6	1247	1	MMHUND nidogen precursor - h	2.42e-02
37	111	3.5	656	2	JC2005 integrin beta-5 chain	6.15e-02
38	111	3.5	1607	1	MMMSB2 lamnln gamma-1 chain	6.15e-02
39	112	3.5	1609	1	MMHUB2 lamnln gamma-1 chain	4.51e-02
40	108	3.4	103	2	A42523 A53R protein - vaccin	1.53e-01
41	110	3.4	289	2	A46515 B cell-associated sur	8.35e-02
42	110	3.4	305	2	A46476 CD40 - mouse	8.35e-02
43	109	3.4	571	2	C75165 glutamyl-tRNA synthet	1.13e-01
44	109	3.4	1790	1	MMFPB1 lamnln beta-1 chain	1.13e-01
45	109	3.4	3707	2	S18252 heparan sulfate prote	1.13e-01

## ALIGNMENTS

RESULT	1	ALIGNMENTS
ENTRY	GOHUT1	#type complete
TITLE	tumor necrosis factor receptor 1 precursor - human	
ALTERNATE_NAMES	P55 tumor necrosis factor receptor; TNF receptor	
CONTAINS	tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein 1 (TNF blocking factor)	
ORGANISM	#formal_name Homo sapiens #common_name man	
DATE	30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 22-Jun-1999	
ACCESSIONS	A38208; A34899; A34900; A36555; A38281; S12057; J07058; A60231; A38258; A60594; A35010; JC2404	
REFERENCE	A38208	
#authors	Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.	
#journal	Genomics (1992) 13:219-224	
#title	Structure of the human TNF receptor 1 (p50) gene (TNRF1) and localization to chromosome 12p13.	
#cross-references	MUID:92250049	
#accession	A38208	
#molecule_type	DNA	
#residues	1-455 #label FUC	
#cross-references	GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AAA61201.1; PID:g339750	
REFERENCE	A34899	
#authors	Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslauer, W.	
#journal	Cell (1990) 61:351-359	
#title	Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor.	
#cross-references	MUID:90235284	
#accession	A34899	
#molecule_type	mRNA	
#residues	1-455 #label LOE	
#cross-references	GB:M58286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754	
#experimental_source	part of this sequence, including the amino end of the mature protein, confirmed by protein sequencing	
#note		
REFERENCE	A34900	
#authors	Schall, T.J.; Lewis, M.; Koller, R.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.; Granger, G.A.; Lentz, R.; Raab, H.; Kohr, W.J.; Goeddel, D.V.	
#journal	Cell (1990) 61:361-370	
#title	Molecular cloning and expression of a receptor for human tumor necrosis factor.	
#cross-references	MUID:90235285	
#accession	A34900	
#molecule_type	mRNA	

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REFERENCE
##residues 1-455 ##label SCH
##cross-references GB:M33294; NID:g339744; PIDN:AAA03210.1; PID:g339745
#authors A36555
#journal Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.;
#title Pfizenmaier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;
Stratowa, C.; Adolf, G.R.
Mol Cell Biol. (1990) 9:705-715
#cross-references NID:91090841
#accession A36555
##molecule_type mRNA
##residues 1-455 ##label HIM
##cross-references GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
#accession C36555
##molecule_type protein
#residues 30-38;41-53,'X',55-79,'XX',82-94,'NK','XX',100-104;
107-128;162-167,'X',169-201 ##label H12
#note the purified protein, called tumor necrosis factor
binding protein, is a soluble derivative of the
receptor
REFERENCE
#authors A38281
#journal Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann,
M.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:7380-7384
#title Cloning of human tumor necrosis factor (TNF) receptor cDNA
and expression of recombinant soluble TNF-binding protein.
#cross-references MUID:91017509
#accession A38281
##molecule_type mRNA
#residues 1-455 ##label GRA
#cross-references GB:M37764
#note the authors translated the codon TGG for residue 371 as
Thr, AAG for residue 372 as Leu, and GAC for residue
427 as Asn
REFERENCE
#authors S12057
#journal Nophrat, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwarg
R.; Aderka, D.; Holtmann, H.; Wallach, D.
EMBO J. (1990) 9:3269-3278
#title Soluble forms of tumor necrosis factor receptors (TNF-Rs) .
The cDNA for the type I TNF-R, cloned using amino acid
sequence data of its soluble form, encodes both the cell
surface and a soluble form of the receptor.
#cross-references MUID:91006021
#accession S12057
##molecule_type mRNA
#residues 1-455 ##label NOP
#cross-references EMBL:X5513; NID:g37223; PIDN:CAA39021.1; PID:g37224
#note parts of soluble TNF binding protein 1, including its
amino and carboxyl ends, were confirmed by protein
sequencing
REFERENCE
#authors JT0758
#journal Kemper, O.; Wallach, D.
Gene (1993) 134:209-216
#title Cloning and partial characterization of the promoter for the
human p55 tumor necrosis factor (TNF) receptor.
#cross-references MUID:94085779
#accession JT0758
##molecule_type DNA
#residues 1-13 ##label KEM
REFERENCE
#authors A60231
#journal Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer,
J.M.
Eur. J. Immunol. (1990) 20:1167-1174
#title Tumor necrosis factor inhibitor: purification, NH-2-terminal
amino acid sequence and evidence for anti-inflammatory and
immunomodulatory activities.
#cross-references MUID:90292116
#accession A60231
##molecule_type protein
#residues 41-43,'X',45-53,'X',55-57 ##label SEC
REFERENCE
A38258

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#authors          #journal          #title          #cross-references MUID:91062364
#accession       A38258
##molecule_type protein
##residues      41-60 ##label GAT
##experimental_source cancer patient serum
REFERENCE
#authors         Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.,
#journal         Eur. J. Haematol. (1989) 42:270-275
#title           Isolation and characterization of a tumor necrosis factor
#binding protein from urine.
#accession       A60594
##molecule_type protein
##residues      41-43, 'X', 45-53, 'V', 55-57, 'XK', 60 ##label OLS
##experimental_source renal failure patient urine
REFERENCE
#authors         Engelmann, H.; Novick, D.; Wallach, D.
#journal         J. Biol. Chem. (1990) 265:1531-1536
#title           Two tumor necrosis factor-binding proteins purified from
#human urine. Evidence for immunological cross-reactivity
#with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession       A35010
##molecule_type protein
##residues      41-45 ##label ENG
##experimental_source normal urine
REFERENCE
#authors         Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
#journal         Biosci. Biotechnol. Biochem. (1994) 58:2266-2268
#title           Amino acid sequence of natural tumor necrosis factor alpha
#inhibitor purified from human urine.
#cross-references MUID:95128033
#accession       JC2404
##molecule_type protein
##residues      41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201
#label KAJ
##experimental_source urine
COMMENT          This protein is one of two known receptors for both TNF-alpha
                  (cachectin) and TNF-beta (lymphotoxin).
GENETICS
#gene            GDB:TNFR1
##cross-references GDB:125913; OMIM:191190
#map_position    12p13.2-12p13.2
#intons          13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
CLASSIFICATION  #superfamily tumor necrosis factor receptor type 1; NCF
                  receptor repeat homology
                  duplication; glycoprotein; receptor; transmembrane protein
KEYWORDS
FEATURE
1-21             #domain signal sequence #status predicted #label SIG\
122-455         #product tumor necrosis factor receptor type 1 #status
                  predicted #label MAT\
30-211          #domain extracellular #status predicted #label EX\
41-201          #product TNF binding protein 1 (tumor necrosis factor
                  alpha inhibitor) #status experimental #label TBP1\
44-82           #domain NCF receptor repeat homology #label NG1\
86-126          #domain NCF receptor repeat homology #label NG2\
127-167         #domain NCF receptor repeat homology #label NG3\
168-196         #domain NCF receptor repeat homology #label NG4\
212-224         #domain transmembrane #status predicted #label MEM\
235-455         #domain intracellular #status predicted #label INT\
54,145,151     #binding site carbohydrate (Asn) (covalent) #status
                  predicted
SUMMARY
#length 455     #molecular-weight 50494 #checksum 153

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Query Match	12.7%	Score 407	DB 1	Length 455
Best Local Similarity	29.9%	Pred. 7.65e-55		
Matches 127	Conservative	81	Mismatches 177	Indels 40
				Gaps 32
Db	27	VIGLVPLHLDREKRDSPGKGYIHPQNNISICCKKCKGTLYLNDCKPGPGDTCRECS	86	
QY	19	LLCARAGGGRSR-CDCA-GDF-HKKIGLFCRCGACAGHTLAKPCTEPCGNSICLVCPQ	75	
Db	87	GSTFASSENHLR-HCLSCSKCKEMGOVEISSCTVDRTYCGCRKNQYRHYW-SENLPQC	143	
QY	76	DIFLANENHHNSCARCQACDQASQVALENCNSAVADTRCGCKRGWVECVQSVSSSP	135	
Db	144	FNCSLCLN-GTYV----LSQEKONTVC-TCHAGFEI.RENECVCSCKSKSECTKLCPL	197	
QY	136	FYCPQPLDGCALRHRTLR-LC-SRRDDCGCLCPPEYEHGGCVCSPTSLG-SCPERC-A	192	
Db	198	QIENVKGTDGSGTTLPL-LVIFGGLCLSLFLGLMYRQRMYSKILSYICGSTPEKE	256	
QY	193	AVCGWQDM-W-VQVLLAGLV--PL-LIGCATLT-LYTR-HCWPHK--PLVTADEA-GME	242	
Db	257	GELEGTTRKPLADPSPFSPTPGFTPLGFSVPVSTFTSSSTYTPGDCPNFAARREYAP	316	
QY	243	A-LTPPAPHLSPLDS-AHTL-LAPDSSSEKICHTVLVQNS-WPQXPEQEAOLCPYT	297	
Db	317	PIQGAPPIATALASDPPIRPLOKMECSAKPOSULTDDPATLYAAVENPPLMKKEVR	376	
QY	298	-W-SWDLPSRLGPAAP-LSP-ESPASPPAMLOPGQ-LYDVADVAPARMKKEVR	352	
Db	377	RGLSHEIDRLRLONGRCLEAOYSMLATWRRTPREATLELGVLRMDLGGLED	436	
QY	353	TIGLRRAELIENAVEVEIGR-FRDOQTEMLKRWROQP--AGLCAYVALERMGIDGVED	408	
Db	437	IEEAL 441		
QY	409	LRSRL 413		
RESULT 2				
ENTRY	GOMST1	#type complete		
TITLE	tumor necrosis factor receptor 1 precursor	- mouse		
ALTERNATE_NAMES	tumor necrosis factor receptor.55k			
ORGANISM	#formal_name Mus musculus	#common_name house mouse		
DATE	30-Jun-1992	#sequence_revision 30-Jun-1992	#text_change 22-Jun-1999	
ACCESSIONS	A38634	B40254	S16677	S19021
REFERENCE	A38634			
#authors	Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.Y.; Goeddel, D.V.			
#journal	Proc. Natl. Acad. Sci. U.S.A.	(1991)	88:2830-2834	
#title	Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.			
#cross-references	MUID:91187885			
#accession	A38634			
#molecule_type	mRNA			
#residues	1-454	##label LEW		
#cross-references	CB:M60468	NID:g199825	PIDN:AAA39751.1	PID:g199826
REFERENCE	A40254			
#authors	Goodwin, R.G.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkins, N.A.; Smith, C.A.			
#journal	Mol. Cell. Biol.	(1991)	11:3020-3026	
#title	Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.			
#cross-references	MUID:91246168			
#accession	B40254			
#molecule_type	mRNA			
#residues	1-454	##label GO2		
#cross-references	KB:M60468	NID:g199825	PIDN:AAA39751.1	PID:g199826
REFERENCE	S16677			
#authors	Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldmann, M.; Foxwell, B.M.J.			
#journal	Eur. J. Immunol.	(1991)	21:1649-1656	
#title	Cloning, expression and cross-linking analysis of the murine			

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p55 tumor necrosis factor receptor.
#cross-references MUID:91285014
#accession S16677
##molecule_type mRNA
##residues 1-454 ##label BAR
REFERENCE
#cross-references EMBL:559238; NID:953578; PIDN:CAAA1922.1; PID:953579
#journal S19021
#authors Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
#journal Immunogenetics (1991) 34:338-340
#title Molecular cloning and expression of the mouse Tnf receptor type b.
#cross-references EMBL:92039815
#accession S19021
##molecule_type mRNA
##residues 1-454 ##label ROT
REFERENCE
#cross-references EMBL:57796; NID:954848; PIDN:CAAA0936.1; PID:954849
#journal 154532
#authors Rebo, B.F.
#journal Immunogenetics (1994) 39:450-451
#title Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell line.
#cross-references MUID:94245292
#accession I54532
##status translated from GB/EMBL/DBU
##molecule_type mRNA
##residues 1-454 ##label RES
#cross-references GB:I26349; NID:9430732; PIDN:AAA59361.1; PID:94307333
COMMENT This protein is one of two distantly related receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).
CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology
KEYWORDS duplication; glycoprotein; receptor; transmembrane protein
FEATURE
1-29 #domain signal sequence #status predicted #label SIG\
30-454 #product tumor necrosis factor receptor type 1 #status predicted #label MAT\
30-212 #domain extracellular #status predicted #label EXT\
44-82 #domain NGF receptor repeat homology #label NG1\
84-136 #domain NGF receptor repeat homology #label NG2\
127-167 #domain NGF receptor repeat homology #label NG3\
168-204 #domain NGF receptor repeat homology #label NG4\
213-235 #domain transmembrane #status predicted #label MEM\
236-454 #domain intracellular #status predicted #label INT\
54,151,202 #binding-site carboxylate (Asn) (covalent) #status predicted
SUMMARY #length 454 #molecular-weight 50129 #checksum 4839
Query Match 12.5%, Score 399; DB 1; Length 454;
Best Local Similarity 28.7%; Pred. No. 2,92e-53;
Matches 119; Conservative 79; Mismatches 182; Indels 34; Gaps 28;
Db 40 RDSICLP-OGKVVHKKNNISICTCKHKGTLYVSOCPSPGRPTVCRECKGTFTASQWYLR- 97
29 RSPRDCAGDE-HKKIGLFCRCGRPAHNYLKAPTECGSTLCVCPDFTFLAMENHNS 87
98 QCLSCGTCRKMSQVEISPCQADKDYCGCKENOFORYLESTHFQCDSCSPCNGTVTTP 157
88 ECARQADDEBQSAQVALENCASAVADTGCCKPGEFTVC--QVS-QCYSSSP-FYQPCLD 143
158 CKETQ-NTVCNCHAGFLRESEVPC--SHCKNEBCMKILCLPPLANTNTPODSTAVL 214
144 CGALHRTLRILC-SR---RDTDCGTCPLRGEYHEDGCVS-CPTSTLQSC--PERCAAVCG 196
215 LPVILGLCLLSTFLFISLMGRYRMKRPVYVSTICRPPV-VKEBKAGK-PLTPASPAF 272
197 WRQMWQVY-LLAGLVYPL-L-LGTYL--TYTYRH-CWPHKPLVYADEGEMPPVATPH 252
273 SPTSGFNFTLGFSPNGSSPVSSRP-ISPFGSPSNHMFMPVSEVYPTQCADPLTESIC 331
253 SPDS-ATTL-LAPDSESKICTYQVLGNSWTPREYPTQALCPQV-TNSMDLPRLAG 309
332 SVPAFTSVQKWEDESAHPQRPDNDALATLVAVVDGVPAPRKKEKMRMGSLSEHIERLEMQ 391

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OY 310 PAAAPTLPSPSPAGS-PAMMLOPG-POLYDVMDAVPARMKFEVETLGLREAEIIEAVEVE 367

Db 392 NGRCLEAOYSMLAEWRRTPRHEDTLEVGLVSKMLAGLENTLEAL-RNP 444

OY 368 IGR-FRDOOYEMLKRWROOP--AG-LGAVYAALERMGLDCEVEDLRSLRQRP 417

RESULT 3

ENTRY JC4302 #type complete

TITLE tumor necrosis factor receptor p55 precursor - pig

ORGANISM #formal\_name Sus scrofa domestica #common\_name domestic pig

DATE 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999

ACCESSIONS JC4302; PC4093

REFERENCE JC4302

#authors Suter, B.; Pauli, U.

#journal Gene (1995) 163:263-266

#title Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.

#cross-references MUID:96011645

#accession JC4302

##molecule\_type mRNA

##residues 1-461 ##label SUR

##cross-references GB:U1994; NID:g1141752; PIDN:AC4849.1; PID:g1141753

#accession PC4093

##molecule\_type protein

##residues 1-7 ##label SU2

##experimental\_source kidney cell line 15

GENETICS

#gene tnfr

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

KEYWORDS glycoprotein; kidney; receptor; transmembrane protein; tumor

FEATURE

1-29

30-461

44-194

44-82

84-126

211-231

361-447

54,145,151

SUMMARY

#length 461 #molecular\_weight 50696 #checksum 8079

Query Match

Best Local Similarity 32.3%; Pred. No. 4,61e-53;

Matches 139; Conservative 81; Mismatches 160; Indels 51; Gaps 32;

Db 33 HPGREKRESICPGGKSHPNRISCTCKHKGYTLHANDCLAGIDTCRECDNFTFAS 92

OY 25 OGGRSR-CPGA-GDF-HKRTGLFCRCGCPAGHYLAKPCTEPCGNSCLVCPDFTFLAM 81

Db 93 ENHT-TOLSCSKRSEKSOYEISPCVDRDYVCGCRKN--QYR-KY-NSETLF-Q-C 143

OY 82 ENHNSECARQACDEQASQVALENCSAVADTRCGCKPGMVEYECOVSOVSSSPFYCOPC 141

Db 144 LNC-SLCPNGTVOLPCELEKODTICN-CHSGFLRDKECVSNCKNADCKNLCPATSETR 201

OY 142 LDGALHRH-T-RLLC-SRBDTDCGLPGFYEHGDCVSCPTSTLIGSCPENCAVCMR 198

Db 202 NDPODTGTVLLPLVIFGLCLAFLEVLGACRIOR-WKPKYLSITGCKSTPVKGEDEP 260

OY 199 QMEF---VOYILA-----GLVVPRLIGATLYTYRHCWPHK--PLY---TA-DEAGMEA 243

Db 261 LATAPSGPITTFSPISPTTPSPVSPSSPFTFCODMSNITVTSPPKRIAPP 320

OY 244 L-TTP---PHTLSPLDS-AHTL-LAPDSSSKICTVOLVGNMTP---GIPETDEALCP 294

Db 321 QGAGILPMPASTVPPTPLPKMGSAHSAPOLADADPATLYAVVGPPTRMKEF 380

OY 295 QYTWEMDQLP-SRALGPAAAPTL--SPSPAGSPAMMLOPGHQ-LYDVMDAVPARMKFE 350

Db 361 VRRLLSEHIEIRLELQNGRCLEAOYSMLAEWRRTSRRETLLELGSVLDMDLGL 440

OY 351 VRTGLREAEIIEAVEVEIGR-FRDOOYEMLKRWROO--OP-AGLAVYAALERMGLDGV 406

Db 441 EDIEBAL-RGP 450

OY 407 EDLRSLRQRP 417

RESULT 4

ENTRY 157826 #type complete

TITLE tumor necrosis factor receptor - mouse

ORGANISM #formal\_name Mus musculus #common\_name house mouse

DATE 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 23-Jul-1999

ACCESSIONS 157826

REFERENCE 157826

#authors Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

#journal Mol. Immunol. (1993) 30:165-176

#title Genomic organization and promoter function of the murine tumor necrosis factor receptor beta gene.

#cross-references MUID:93156721

#accession 157826

##status preliminary; translated from GB/EMBL/DBDJ

##molecule\_type DNA

##residues 1-454 ##label RES

##cross-references GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102

GENETICS

#gene TNFR-2

CLASSIFICATION #superfamily tumor necrosis factor receptor type 1; NGF receptor repeat homology

KEYWORDS cytokine receptor

FEATURE

44-82

SUMMARY

#length 454 #molecular\_weight 50030 #checksum 4267

Query Match

Best Local Similarity 28.5%; Pred. No. 1,68e-50;

Matches 118; Conservative 79; Mismatches 183; Indels 34; Gaps 28;

Db 40 RDSLCP-QGKYVHSKNNISCTCKHKGYTLVSDCPSPGMDYCRBEKGTFTASQVLYR- 97

OY 29 RSPRCDACGDF-HKRTGLFCRCGCPAGHYLAKPCTEPCGNSCLVCPDFTFLAMENHNS 87

Db 98 OLSGCTCKREMSQYEISPCQADKDTVCGCKENOFQRYLSETHFOCVDCSPFNGTVTIP 157

OY 88 ECARQACDEQASQVALENCSAVADTRCGCKPGMVEYEC--QYS-QCVSSP-FYCGPCID 143

Db 158 CKETO-NIVCNCHAGFLESECVPC--SHCKNNECMKLCPLRPPLANTNPQDSTAVL 214

OY 144 CGALHRHETRLC-SR---RDTDCGTCPLPGFYEHGDCVCS-CPTSTIGSC--PERCAAYCG 196

Db 215 LPLVILIGLCLSFIFISIMCYPRMRPRVYSTICDPRP-VKEEKAG-PLTPAPSPAF 272

OY 197 WHOMFWVOY-LLAGLVPL-LGATL-TYTYRN-CWPHKPLVTADAGMALPRPTATP 252

Db 273 SPTSGFNPTLPGTSPGSSPVASTP-ISPIFGPSMNHMPRVSEVVPOTGADPLYESIC 331

OY 253 SPLDS-AHTL-LAPDSSSKICTVOLVGNMTPRGYETDEALCPQV-TSMWQLPBRALG 309

Db 332 SVAPLTVOQKWDASHPPORDNADLAIIYAVVDGVPAPAKEMRPMGLSEHIEIRLEMO 391

OY 310 PAAAPTLPSPSPAGS-PAMMLOPG-POLYDVMDAVPARMKFEVETLGLREAEIIEAVEVE 367

Db 392 NGRCLEAOYSMLAEWRRTPRHEDTLEVGLVSKMLAGLENTLEAL-RNP 444

OY 368 IGR-FRDOOYEMLKRWROOP--AG-LGAVYAALERMGLDCEVEDLRSLRQRP 417

RESULT	5	
ENTRY	GORTT1	#type complete
TITLE	tumor necrosis factor receptor 1 precursor - rat	
CONTAINS	tumor necrosis factor binding protein 1 (TNF blocking factor	
ORGANISM	#formal_name Rattus norvegicus #common_name Norway rat	
DATE	30-Jun-1992	#sequence_revision 07-Oct-1994
	22-Jun-1999	#text_change
ACCESSIONS	B36555	
REFERENCE	A36555	
authors	Himmler, A.; Maurer-Fogy, I.; Kroecken, M.; Scheurich, P.; Plitzemaeier, K.; Lantz, M.; Olsson, I.; Hauptmann, R.;	
#journal	Stratowa, C.; Adolf, G.R.	
#title	DNA Cell Biol. (1990) 9:705-715	
	Molecular cloning and expression of human and rat tumor	
	necrosis factor receptor chain (p60) and its soluble	
	derivative, tumor necrosis factor-binding protein.	
	derivative, MUID:91090841	
#cross-references	MUID:91090841	
#accession	B36555	
#molecule_type	mRNA	
#residues	1-461	#label HIM
#cross-references	GB:M63122; NID:g207361; PIDN:AAA42256.1; PID:g207362	
COMMENT	This protein is one of two known receptors for both TNF-alpha	
	(cachectin) and TNF-beta (lymphotoxin).	
CLASSIFICATION	#superfamily tumor necrosis factor receptor type 1; NGF	
	receptor repeat homology	
	duplication; glycoprotein; receptor; transmembrane protein	
KEYWORDS		
FEATURE		
1-29		#domain signal sequence #status predicted #label SIG\
30-461		#product tumor necrosis factor receptor type 1 #status
		predicted #label MAP\
30-211		#domain extracellular #status predicted #label EXT\
30-201		#product tumor necrosis factor binding protein #status
		predicted #label TBP\
44-82		#domain NGF receptor repeat homology #label NG1\
84-126		#domain NGF receptor repeat homology #label NG2\
127-167		#domain NGF receptor repeat homology #label NG3\
168-204		#domain NGF receptor repeat homology #label NG4\
212-234		#domain transmembrane #status predicted #label MEM\
235-461		#domain intracellular #status predicted #label INT\
54,151,201		#binding_site carbohydrate (Asn) (covalent) #status
		predicted
SUMMARY	#length 461 #molecular_weight 50969 #checksum 1617	
Query Match	12.0%; Score 383; DR 1; Length 461;	
Best Local Similarity	29.8%; Pred. No. 4.15e-50;	
Matches 125; Conservative 73; Mismatches 185; Indels 37; Gaps 31;		
Db	35 GDREKRNLCPOGKGYAHPKNNKSIICFTGCHGTYLVSPSPGOETVCEVCDKGTFTASON 94	
-Oy	27 GTRSPROD-CA-GDF-HKIGILFCRCRCPAGHYLAKACTEPCGNSCTICVPOQFIAMEN 83	
Db	95 H-VROGLSKCTCKREMDPOVELSPCKADMDTVCGCKKNGFORITLSETHFOCVDCSPCFNGT 153	
Oy	84 HHNSCARCOACDQASOVALENCSAAVDPRCGCKPQWPEVC--QVS-QCVSSP-FYCO 139	
Db	154 VTIPKE-KONTVONCHAGFFLSENETPCSHCKKCKEKKLLDPRANTYNQDSGTAV 212	
Oy	140 PCLDQGAHHRTRILCLSRDTGCT-CLP-GFYEHGAGCVS-C-PTSTGASCPERCACAVC 195	
Db	213 LPLVFLGLCLFFICISLCLRPQWRPRYSITICRDSAPVKEVEGEGIVTPRLPAST 272	
Oy	196 GMRQEFVQV-LLAGIVPLL-LGATLTYTYRH-CPRHKPLVTADACG--EALTRPPA 249	
Db	273 PAFSPNPFENFTLOFSTTPRFSHYVSTPLSPVFGSNNHNFVPVYREVPTO-G-A-DP 329	
Oy	250 THLSPLDS-AHTL-LAP-PDSEKICTVOL--V-GNS-WTPGVPEFOEALCPVTSWQ 302	
Db	330 LLYGLSLNVLPAPVARKMEDVVAQORPLTADPAMLYAVDVDPPLRKMEFRRLGLSE 389	
Oy	303 LPSRALGPAAPLT-LSP-ESPAGSPAMMDPG-PQ-LTYDMADVAPARKMEFVRLTGLSE 358	

Db	390	HELETERLENGCIGRAHYSMLEARRPRPHRATLDVVRVLCDDMLRGLREIRETLE	449
Oy	359	AELEAVEVEIGR-FRQOQYEMLRKRRHOOP--AGIGAVYALERMGLDGCVEDLRSLQ	414
RESULT	6		
ENTRY		JC2395	#type complete
TITLE		Fas antigen precursor - rat	
ORGANISM		#formal_name Rattus norvegicus #common_name Norway rat	
DATE		20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Jul-1999	
ACCESSIONS		JC2395; PC2246	
REFERENCE		JC2395	
#authors		Kimura, K.; Wakatsuki, T.; Yamamoto, M.	
#journal		Biochem. Biophys. Res. Commun. (1994) 198:666-674	
#title		A variant mRNA species encoding a truncated form of Fas antigen in the rat liver.	
#cross-references		NCBI:94128114	
#accession		JC2395	
#molecule_type		mRNA	
#residues		1-324	#label KIM
#cross-references		DBJ:D26113; NID:9468486; PID:d1005650; PID:9468487	
#experimental_source		thymus	
#accession		PC2246	
#molecule_type		mRNA	
#residues		1-62	#label KIT
#cross-references		DBJ:D26113; NID:9468488; PID:d1005651; PID:9468489	
#experimental_source		liver	
GENETICS			
#introns		62/1	
CLASSIFICATION		superfamily NCF receptor repeat homology	
KEYWORDS		transmembrane protein	
FEATURE			
1-21		domain signal sequence	#status predicted #label SIG\
23-324		product Fas antigen	#status predicted #label MAT\
44-79		domain NCF receptor repeat homology	#label NCF\
81-124		domain NCF receptor repeat homology	#label NG4\
171-188		domain transmembrane	#status predicted #label TMM
SUMMARY		#length 324 #molecular_weight 36835 #checksum 7305	
Query Match		6.6%; Score 211; DB 2; Length 324;	
Best local similarity		30.1%; Pred. No. 8,54e-18;	
Matches		37; Conservative 26; Mismatches 47; Indels 13; Gaps 12;	
Db	43	NCSEGLYQ-VGPFCCPCPCPGERKRYD-CTTSGAPCTCHPCTGEEYTDK-KHYSDCRR	99
Oy	34	DCAGDFHKHIGLFCGCGPAG-HYLEAPCTEPCGNTCLVCPQ-DPLFLAMNHNNSCAR	91
Db	100	CAFCEBGHGLEVE-TNCTPTONTKCKCKENFY--CNASLDC-DHC-YHCTSCGLE-DILEP	153
Oy	92	COACDE-QASQVALENCASVADTRCCCKRGWFEYECGVSCVSSSPFYCOPC-LDCGALHR	149
Db	154	CTR 156	
Oy	150	HTR 152	
RESULT	7		
ENTRY		A46484	#type complete
TITLE		apoptosis-mediating membrane-associated polypeptide Fas - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999	
ACCESSIONS		A46484; A47254	
REFERENCE		A46484	
#authors		Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.;	
#journal		Copeland, N.G.; Jenkins, N.A.; Nagata, S.	
#title		J. Immunol. (1992) 148:1274-1279	
#cross-references		NCBI:92148151	
#accession		A46484	

```

##status      preliminary
##molecule_type  mRNA
##residues    1-327 ##label  WAT
##cross-references  GB:M83649; NID:g193225; PID:g193226
##experimental_source  BAM3 macrophage cell line
##note        sequence extracted from NCBI Backbone (NCBIN:81544,
NCBIP:81545)

REFERENCE      A47254
#authors      Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1756-1760
#title        Aberrant transcription caused by the insertion of an early
transposable element in an intron of the Fas antigen gene
of 1pr mice.
#cross-references  MUID:93189576
#accession    A47254
##status      preliminary
##molecule_type  nucleic acid
##residues    1-96 ##label  ADA
##cross-references  GB:S56490; NID:g298505; PID:g298506
##experimental_source  MRL 1pr/1pr
##note        sequence extracted from NCBI backbone (NCBIN:126850,
NCBIN:126853, NCBIN:126863, NCBIP:126864)

CLASSIFICATION  #superfamily NGR receptor repeat homology
KEYWORDS        transmembrane protein
FEATURE
44-79           #domain NGR receptor repeat homology #label NGR\
81-124          #domain NGR receptor repeat homology #label NG4
SUMMARY         #length 327 #molecular-weight 37417 #checksum 8479

Query Match      6.4%; Score 204; DB 2; Length 327;
Best Local Similarity 27.9%; Pred. No. 1,42e-16;
Matches 29; Conservative 19; Mismatches 52; Indels 4; Gaps 4;

Db      43 NCSEGLYG-GPFCOPCPGKRRVDECKNNGSTPTCAPCTEKEYMD-KNHADKCRRC 100
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Oy      34 DCAGDFHKKIGLFCGCGCPAGHYLKARCTERCNSTCLVCPQDT-FLAWENHHNSECARC 92
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:

Db      101 TLCDDEHGLEVEETNCTLNTONTKCKRPFDFCGSGEHCRCAS 144
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Oy      93 QACDEQASQVALENCASAVADTRCGKRFGWFEQVVS-QCVSSSP 135
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:

RESULT      8
ENTRY
TITLE      137383 #type complete
ORGANISM   FAS soluble protein - human
DATE       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
ACCESSIONS 137383
REFERENCE  137383
#authors   Cascino, I.; Flincci, G.; Papoff, G.; Ruberti, G.
#journal   J. Immunol. (1995) 154:2706-2713
#title     Three functional soluble forms of the human
apoptosis-inducing Fas molecule are produced by alternative
splicing.
#cross-references  MUID:95181785
#accession    I37383
##status      preliminary; translated from GB/EMBL/DBJ
##molecule_type  mRNA
##residues    1-314 ##label  RES
#cross-references  EMBL:Z47993; NID:g728578; PID:g695359
SUMMARY         #length 314 #molecular-weight 35386 #checksum 655

Query Match      5.9%; Score 190; DB 2; Length 314;
Best Local Similarity 34.1%; Pred. No. 3.66e-14;
Matches 31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

Db      56 GQCFHRCPPGGE-RKARDCTVNGDEPDPCVQEGKEYTD-KAHSSKCRRCRLDDEGHGL 113
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:
Oy      44 GLECCRCGCPAGHYLKAP-CTEPCGNSTCLVCPQDT-FLAWENHHNSECARCQACDE-QAS 100
      11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11: 11:

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Yy      101 QVALENCSAVADTRCGCKRPGMFVEQGVs-OC 130

RESULT          9
ENTRY           A40036 #type complete
TITLE           apoptosis-mediating surface antigen Fas precursor - human
ALTERNATE_NAMES surface antigen Apo-1
ORGANISM        #formal_name Homo sapiens #common_name man
DATE            17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change
                10-Sep-1997

ACCESSIONS      A40036; S24543; A38142
REFERENCE       A40036
#authors        Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima,
                S.-I.; Sameshima, M.; Hase, A.; Seto, Y.; Nagata, S.
#journal        Cell (1991) 66:233-243
#title          The polypeptide encoded by the cDNA for human cell surface
                antigen Fas can mediate apoptosis.
#cross-references MIMD:J1309137
#accession      A40036
#status         preliminary
#molecule_type mRNA
##residues      1-335 ##label ITO
REFERENCE       S24543
#cross-references GB:M67454; NID:g182409; PID:g182410
#accession      S24543
#status         submitted to the EMBL Data Library, February 1992
#submission     Krammer, P.H.
#accession      S24543
#status         preliminary
#molecule_type mRNA
##residues      1-335 ##label KRA
#cross-references EMBL:X63717; NID:g28741; PID:g28742
REFERENCE       A38142
#authors        Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.;
                Blas, C.; Li-Weber, M.; Richards, S.; Dhein, J.; Trauth,
                B.C.; Ponstingl, H.; Krammer, P.H.
#journal        J. Biol. Chem. (1992) 267:10709-10715
#title          Purification and molecular cloning of the Apo-1 cell surface
                antigen, a member of the tumor necrosis factor/nerve growth
                factor receptor superfamily. Sequence identity with the Fas
                antigen.
#cross-references MIMD:92268122
#accession      A38142
#status         preliminary; not compared with conceptual translation
#molecule_type nucleic acid
##residues      1-134 /Q/, 136-335 ##label OEH
#experimental_source SKW6.4 cells
#note           sequence extracted from NCBI backbone (NCBIP:103810)
                in NCBI backbone the source is designated as mouse
GENETICS        #note
#gene           GDB:APT1
#cross-references GDB:132671; OMIM:134637
#map_position   10q24.1-10q24.1
CLASSIFICATION #superfamily NGF receptor repeat homology
KEYWORDS        apoptosis; surface antigen; transmembrane protein
FEATURE         #domain signal sequence #status predicted #label SIG\
                85-128 #domain NCF receptor repeat homology #label NG4\
                174-190 #domain transmembrane #status predicted #label TMM
SUMMARY         #length 335 #molecular-weight 37732 #checksum 4899

Query Match      5.9%; Score 190; DB 2; Length 335;
Best local Similarity 34.1%; Pred. No. 3.60e-14;
Matches          31; Conservative 18; Mismatches 35; Indels 7; Gaps 7;

Db      56 GCPCHRPCCPGE-RKARDCTVNGDEPDPCVCQGSKETTD-KAFSSKCRGRCLCDEHGL 113
        1 11 : 11 : 1 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
Qy      44 GLFCGRCGPAGHYLKAP-CTEPCGNSTCLVCPDDT-FLAMENHNSECARQCACDE-QAS 100
        : : : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
Db      114 EVEI-NCTRTQNTCKRCKRPNFCNSTCYEHC 143
        : : : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 : 11 :
Qy      101 QVALENCSAVADTRCGCKRPGMFVEQGVs-OC 130

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REFERENCE      S32385
#authors       ShchelI'kunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
#journal        FEBS Lett. (1993) 319:80-83
#title          Genes of variola and vaccinia viruses necessary to overcome
                the host protective mechanisms.
#cross-references MUID:93202281
#accession      S32385
#molecule_type DNA
#residues       31-168 #label SHC
##cross-references EMBL:X69198
##experimental_source strain India-1967, ssp. major

GENETICS
#gene           G4R
CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat
               homology

FEATURE
32-66          #domain NGF receptor repeat homology #label NGF\
68-109         #domain NGF receptor repeat homology #label NG2\
110-151        #domain NGF receptor repeat homology #label NG3
SUMMARY
Query Match    5.6%; Score 179; DB 2; Length 349;
Best Local Similarity 27.1%; Pred. No. 2,56e-12;
Matches 29; Conservative 27; Mismatches 43; Indels 8; Gaps 7;

Db   15 IINGRDAPPTPENGKCKDTEY-KRHNL-CCLSCPGTYASRLC-DSKTNTOCTPCGSG 71
     ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy   18 VLICGARAGCGTRSPRCDC-ACDPFKIKITGLFCRCRGCPAGHYLKAPCRPCGNSTCYLPQD 76
     |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   72 TFTSNNHNL-PALCSNGRCN-SNOVETRSCNTNHRICECSFGY 115
     ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy   77 TFLAMENHNHSECARCOA-CDEQASQVALENCASAVADTRCGCKRFGWPF 122

RESULT 12
ENTRY    A46517 #type complete
TITLE    CD27 antigen precursor - human
ALTNAME  CD27L receptor; T cell activation antigen CD27
ORGANISM Homo sapiens #common.name man
DATE     18-Jun-1993 #sequence_revision 22-Apr-1995 #text_change
        22-Jun-1999

ACCESSIONS
REFERENCE A46517; A46454
#authors  Loenen, W.A.; Gravesstein, L.A.; Beuner, S.; Meljief, C.J.;
        Hagemeijer, A.; Borst, J.
#journal  J. Immunol. (1992) 149:3937-3943
#title    Genomic organization and chromosomal localization of the
        human CD27 gene.
#cross-references MUID:93094588
#accession A46517
#status     not compared with conceptual translation
##molecule_type DNA
##residues 1-260 ##label LOE
#note       Sequence extracted from NCBI backbone (NCBIP:120386)
        authors propose an alternative repeat pattern
REFERENCE    A46454
#authors     Cammerlind, D.; Walz, G.; Loenen, W.A.; Borst, J.; Seed, B.
#journal      J. Immunol. (1991) 147:3165-3169
#title        The T cell activation antigen CD27 is a member of the nerve
        growth factor/Tumor necrosis factor receptor gene family.
#cross-references MUID:92013149
#accession    A46454
#molecule_type mRNA
##residues    1-58, 'A',60-260 #label CAM
##cross-references GB:M63928; NID:g180084; PIDN:AA58411.1; PTD:g180085S
        sequence extracted from NCBI backbone (NCBIN:60285,
        NCBIP:60289)

COMMENT      A soluble CD27 found in serum and urine is formed by proteolysis.
GENETICS
#gene         GDB:CD27
#cross-references GDB:132582; OMIM:186711
#map_position 12p13-12p13
#introns      46/1; 90/1; 150/1; 180/1; 220/1

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CLASSIFICATION
KEYWORDS
#superfamily CD27 antigen; NGF receptor repeat homology
duplication; glycoprotein; homodimer; phosphoprotein;
receptor; surface antigen; T-cell; transmembrane protein

FEATURE
1-20
21-260
21-191
27-63
65-105
121-188
192-211
212-260
95
#domain signal sequence #status predicted #label SIG\
#product CD27 antigen #status predicted #label MAR\
#domain extracellular #status predicted #label EXT\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#region proline/serine/threonine-rich\
#domain transmembrane #status predicted #label TMN\
#domain intracellular #status predicted #label INT\
#binding_site carbohydrate (Asn) (covalent) #status
predicted

SUMMARY
#length 260 #molecular-weight 29186 #checksum 1652

Query Match 5.4%; Score 174; DB 1; Length 260;
Best Local Similarity 25.4%; Pred. No. 1,73e-11;
Matches 31; Conservative 34; Mismatches 48; Indels 9; Gaps 7;

Db 9 LCVLGTLVGLSTAPRK-SCPERHWAGKLCOMCEPFTLVKDCDOHNRKTAQCPICP 67
| : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 17 LVLLDA-RAQGTGRSPRCACADDFHKIGLFCRCGRPACHYLAKPTECGNSTCLVC-P 74
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 68 GVSFSP-DHNRPRHCESRHCN--SGLL-VRNCTITANAECACRNGW--QCRDKETED 121
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 75 ODTFLAEMHNHSECARCQACDQASQVALIENCSAVALDTRCGCKPGMFEQGVQSVCS 134

Db 122 PL 123
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 135 PR 136

RESULT 13
ENTRY A35356 #type complete
TITLE tumor necrosis factor receptor type 2 precursor - human
ALTERNATE_NAMES 75K tumor necrosis factor receptor
ORGANISM #formal_name Homo sapiens #common_name man
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
10-Sep-1999
ACCESSIONS A35356; A36475; A48416; A36007; A23666; B35010; I38094
A35356
REFERENCE
#authors Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann,
M.P.; Jerry, R.; Donner, S.K.; Cosman, D.; Goodwin, R.G.
Science (1990) 248:1019-1023
#journal A receptor for tumor necrosis factor defines an unusual
#title family of cellular and viral proteins.
#cross-references MUID:90260639
#accession A35356
#status preliminary
##molecule_type mRNA
##residues 1-461 ##label SMT
##cross-references GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
A36475
REFERENCE
#authors Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King,
M.W.; Hale, K.K.; Squires, C.H.; Thompson, R.C.; Vannice,
J.L. Proc. Natl. Acad. Sci. U.S.A. (1990) 87:8331-8335
#journal A second tumor necrosis factor receptor gene product can shed
#title a naturally occurring tumor necrosis factor inhibitor.
#cross-references MUID:91045991
#accession A36475
#status preliminary
##molecule_type mRNA
##residues 1-195, 'R', 197-461 ##label KOH
##cross-references GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1;
PID:g339758
REFERENCE
#authors Dembic, Z.; Loebscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.;
Gentz, R.; Roetschhaus, M.; Lesslauer, W.
Cytokine (1990) 2:231-237
#journal Two human TNF receptors have similar extracellular, but
#title distinct intracellular, domain sequences.

```

```

#cross-references MUID:91370690
#accession A48416
#status preliminary
#molecule_type mRNA; protein
#residues 23-461 ##label DEM
#cross-references GB:S63366; NID:g235648; PIDN:AA819824.1; PID:g235649
##note sequence extracted from NCBI backbone (NCBIN:63368,
NCBP:63371)

REFERENCE
#authors Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang,
D.; Ringold, G.M.
#journal Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6151-6155
#title Complementary DNA cloning of a receptor for tumor necrosis
factor and demonstration of a shed form of the receptor.
#cross-references MUID:90349572
#accession A36007
#status preliminary
#molecule_type mRNA
#residues 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 ##label HEL
#cross-references GB:M35857; NID:g339751; PIDN:AA63262.1; PID:g339752
#accession A23666
#authors Loeschner, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.;
Lessner, W.; Broekhaus, M.
#journal J. Biol. Chem. (1990) 265:20131-20138
#title Purification and partial amino acid sequence analysis of two
distinct tumor necrosis factor receptors from H160 cells.
#cross-references MUID:91056048
#accession A23666
#status preliminary
#molecule_type protein
#residues 23-40; 65-69; 136-141; 300-306 ##label LOE

REFERENCE
#authors Engelmann, H.; Novick, D.; Wallach, D.
#journal J. Biol. Chem. (1990) 265:1531-1536
#title Two tumor necrosis factor-binding proteins purified from
human urine. Evidence for immunological cross-reactivity
with cell surface tumor necrosis factor receptors.
#cross-references MUID:90110215
#accession B35010
#status preliminary
#molecule_type protein
#residues 27-31 ##label ENG

REFERENCE
#authors Kuhnert, P.; Kemper, O.; Wallach, D.
#journal Gene (1994) 150:381-386
#title Cloning, sequencing and partial functional characterization
of the 5' region of the human p75 tumor necrosis factor
receptor-encoding gene (TNF-R).
#cross-references MUID:95121934
#accession I38094
#status preliminary; translated from GB/EMBL/DBJ
#molecule_type DNA
#residues 1-37 ##label RES
#cross-references EMBL:X80021; NID:g666044; PIDN:CA56324.1;
PID:g825701

GENETICS
#gene GDB:TNFR2
#cross-references GDB:125914; OMIM:191191
#map_position 1p36.2-1p36.2
#introns 26/3
#note the list of introns is incomplete
CLASSIFICATION
#superfamily tumor necrosis factor receptor type 2; NGF
receptor repeat homology
duplication; glycoprotein; receptor; transmembrane protein

KEYWORDS
#domain signal sequence #status predicted #label SIG\
#product tumor necrosis factor receptor type 2 #status
experimental #label MAT\
#domain NGF receptor repeat homology #label NG1\
#domain NGF receptor repeat homology #label NG2\
#domain NGF receptor repeat homology #label NG3\
#domain NGF receptor repeat homology #label NG4\
#domain Transmembrane #status predicted #label TM\

FEATURE
1-22
23-416
40-76
78-119
120-162
164-201
262-279

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280-461      #domain intracellular #status predicted #label IMF\
171,193      #binding_site carbohydrate (Asn) (covalent) #status
SUMMARY      #length 461 #molecular-weight 48291 #checksum 57224

Query Match      5.3%; Score 168; DB 1; Length 461;
Best Local Similarity 27.6%; Pred. No. 1,67e-10;
Matches 24; Conservative 19; Mismatches 37; Indels 7; Gaps 6;

Db 44 EYDQTAQMCCSKSPQAHAKVECTKT-SDTVCDSCEDSTVYTOLM-NW-VPECLSGSRC 100
       ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 38 DEHKIKIGLFECRCRCPAGHYLKAPTEPCGNSITLCVPQDTFFLA-WENHHNSECARQA-C 95
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 101 S--SDQVETQACTREONRICTCRPGWT 125
        :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 96 DEQASQVALENCASAVADTRCGCKRGWF 122

RESULT 14
ENTRY   S12783      #type complete
TITLE   OX40 antigen precursor - rat
ALTERNATE_NAMES
ORGANISM    nerve growth factor receptor homolog
            #format.name Rattus norvegicus #common.name Norway rat
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
           20-Sep-1999
ACCESSIONS S12783; 508036
REFERENCE   S12783
          #authors Mallett, S.; Fossum, S.; Barclay, A.N.
          #journal EMBO J. (1990) 9:1063-1068
          #title Characterization of the MRC OX40 antigen of activated CD4
                  positive T lymphocytes - a molecule related to nerve growth
                  factor receptor.
#cross-references MIMID:90214614
#accession S12783
#molecule_type mRNA
#residues 1-271 ##label MAL
CLASSIFICATION ##cross-references EMBL:X17037; NID:g57830; PID:g57831
KEYWORDS      #superfamily CD27 antigen; NCR receptor repeat homology
              growth factor receptor; transmembrane protein
FEATURE
1-19         #domain signal sequence #status predicted #label SIG\
20-271       #product OX40 antigen #status predicted #label MAY\
211-225      #domain transmembrane #status predicted #label TM\
SUMMARY      #length 271 #molecular-weight 29895 #checksum 379

Query Match      5.2%; Score 165; DB 2; Length 271;
Best Local Similarity 29.7%; Pred. No. 5,14e-10;
Matches 22; Conservative 17; Mismatches 32; Indels 3; Gaps 3;

Db 37 CCRECPGHGMVSR-C-DHTRDTVCVHC-BEPGYN-EAVNYDTCKOSTCNRSGSELKN 93
       |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 47 CCRGCAGHYILKAPTEPCGNSITLCVPQDTFLAEMHNHSECARQACDEQASQVALEN 106
       :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Db 94 CMPTEDTVCCCRPG 107
       |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 107 CSAVADTRCGCKRG 120

RESULT 15
ENTRY   B43692      #type complete
TITLE   T2 protein - rabbit fibroma virus
ALTERNATE_NAMES
ORGANISM    #format.name rabbit fibroma virus, Shope fibroma virus
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
           07-May-1999
ACCESSIONS B43692
REFERENCE   B43692
          #authors Upton, C.; Delange, A.M.; McFadden, G.
          #journal Virology (1987) 160:20-30
          #title Tumorigenic poxviruses: genomic organization and DNA sequence
                  of the telomeric region of the Shope fibroma virus genome.
#cross-references MIMID:87321103
#accession B43692
#status preliminary

```

```
##molecule_type DNA
##residues 1-325 ##label UPT
##cross-references GB:M17433

CLASSIFICATION #superfamily myxoma virus T2 protein; NGF receptor repeat homology

FEATURE
64-105          domain NGF receptor repeat homology #label NG2\
106-147         #domain NGF receptor repeat homology #label NG3
SUMMARY        #length 325 #molecular-weight 35132 #checksum 4629

Query Match      5 1%; Score 164; DB 2; Length 325;
Best Local Similarity 33.0%; Pred. No. 7,46e-10;
Matches    29; Conservative 15; Mismatches 36; Indels   8; Gaps

Db       28 CGGHDEKD-GL-CGASCHPQFYASRLCG-PGSNTVPSPEDCGTFTA-STNHAPACYSKR 83
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy       35 CAG-DFFKKIGLEFCRCGRPGAHYLLKARCTPCGCNSTGLVCPODTFLAMENHHNSECARCQ 93
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db       84 GRPTGNHSE-S-QPCDRTHDVCSNSG 109
           | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Oy       94 A-CDEQASQAILENCMSAVADTRCCCKPR 120
```

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Search completed: Tue Jul 25 22:24:41 2000
Job time : 25 secs.
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Tabular output not generated.

**Sequence:**

### Scoring table:

Searched:

### Statistics:

and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	3198	100.0	417	1	W51517	Death domain containin	6.61e-30
2	3198	100.0	417	1	W95538	Death domain containin	6.61e-30
3	3198	100.0	417	1	W57045	Human apoptosis induci	6.61e-30
4	3198	100.0	417	1	W26709	Human apoptosis protei	6.61e-30
5	3198	100.0	833	1	W64486	Human DR3 protein.	6.61e-30
6	3118	97.5	428	1	W31516	Death domain containin	6.01e-29
7	3118	97.5	428	1	W95537	Death domain containin	6.01e-29
8	1962	61.4	411	1	W57048	Mouse apoptosis induci	2.99e-17
9	1422	44.5	181	1	W26708	Human apoptosis protei	5.28e-12
10	503	15.7	65	1	W93610	Human DR3 protein frag	6.46e-35
11	412	12.9	909	1	W64485	Human Fas protein.	5.05e-26
12	408	12.8	455	1	R07451	Human Tumour Necrosis	5.05e-26
13	407	12.7	455	1	R10986	30kD TNF-inhibitor pre	6.26e-26
14	407	12.7	455	1	R75084	p55 TNF-R.	6.26e-26
15	407	12.7	455	1	R42039	Lambda derived TNF-R.	6.26e-26
16	404	12.6	455	1	R11082	Human 55kD TNF-binding	1.19e-25
17	404	12.6	455	1	R20787	TNF-alpha binding prot	1.19e-25
18	400	12.5	443	1	R51033	Mutant p55 tumour necr	2.79e-25
19	400	12.5	455	1	R51034	Mutant p55 tumour necr	2.79e-25
20	400	12.5	455	1	R42197	p55 Tumour necrosis fa	1.00e-24
21	394	12.3	455	1	R12550	Type I TNF receptor.	4.46e-22
22	387	12.1	433	1	R51032	Mutant p55 tumour necr	1.08e-22
23	372	11.6	455	1	R40000	TNF-alpha 55kD recepto	1.08e-22

[illegible]

## ALIGNMENTS

RESULT	1	
ID	W31517	standard; Protein; 417 AA.
AC	W31517	
DT	02-MAR-1998	(first entry)
DE	Death domain containing receptor DR3.	
KW	Death domain containing receptor; DR3-V1; human; apoptosis; inflammation; NF-kappaB.	
KW	Homo sapiens.	
OS	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Peptide	1..24
FT		/label= Sig-peptide
FT	Domain	25-201
FT		/note= "extracellular domain"
FT	Domain	202..224
FT		/note= "transmembrane domain"
FT	Domain	225..417
FT		/note= "intracellular domain"
FT	Domain	342..408
FT		/note= "death domain"
PN	W09733904-A1.	
PD	18-SEP-1997.	
PF	17-OCT-1996; U16849.	
PR	12-MAR-1996; US-013285.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PA	(UNMT) UNIV MICHIGAN.	
PI	Dillon PJ, Dixit VM, Gentz RL, Ni J, Yu G;	
DR	WPI; 97-470812/43.	
DR	N-PSDB; T89427.	
PT	Death domain containing receptor polypeptide(s) DR3 and DR3-V1 -	
PT	for activation of apoptosis and NF-kappaB, antagonists can be used	
PT	to treat inflammatory diseases	
PS	Claim 1; Page 75-77; 108pp; English.	
CC	This protein comprises human death domain containing receptor	
CC	DR3, a novel member of the tumour necrosis factor receptor	
CC	family. Its amino acid sequence was deduced from a cDNA clone	
CC	(see T89427) isolated from a HVEC cDNA library. Related death	
CC	domain containing receptor DR3-V1 (see W31516) has also been	
CC	identified. Recombinant full-length or mature DR3, or the	
CC	extracellular, transmembrane, intracellular or death domain of	
CC	DR3 can be expressed in transformed host cells. These polypeptides	
CC	can be used to treat diseases and disorders associated with the	
CC	inhibition of apoptosis, or to screen for modulator compounds.	
CC	Antagonists, such as antibodies raised against DR3-V1, can be used	
CC	to treat diseases and disorders associated with increased apoptosis	
CC	and for treating inflammatory diseases and disorders.	
SQ	Sequence 417 AA;	

Query Match	100.0%	Score 3198	DB 1	Length 417
Best Local Similarity 100.0%		Pred. No. 6,616-300		
Matches 417	Conservative	0	Mismatches 0	Indels 0
				Gaps 0
Db	1	MEORRGCAAAVAAALLVLLGARAAGGTRSPRCACAGPFHKKIGLFFCCRGCPAGHYLKAP	60	
Qy	1	MEORRGCAAAVAAALLVLLGARAAGGTRSPRCACAGPFHKKIGLFFCCRGCPAGHYLKAP	60	
Db	61	CTEPGCGNSTCLVCPQDPTFLAENHHNSCANCQAQCDQASVAALENCSAAVDTRCGKPG	120	
Qy	61	CTEPGCGNSTCLVCPQDPTFLAENHHNSCANCQAQCDQASVAALENCSAAVDTRCGKPG	120	
-Db	121	WFEVCOVSQCVSSSPFYQCPLDCGALRRHRLILCSRDDTCGTLPGFYEHDGCVSCP	180	
Qy	121	WFEVCOVSQCVSSSPFYQCPLDCGALRRHRLILCSRDDTCGTLPGFYEHDGCVSCP	180	
Db	181	TSTLGSCEPCAAVCGMROMFVVOYVLLAGVPLILGATLTYTRHCPHKEPLVTADEAG	240	
Qy	181	TSTLGSCEPCAAVCGMROMFVVOYVLLAGVPLILGATLTYTRHCPHKEPLVTADEAG	240	
Db	241	MEALPPPATHTLSPDASHHTLLAPDSESEKICTVOVGNSTMPGYPTFOALACQVYMSW	300	
Qy	241	MEALPPPATHTLSPDASHHTLLAPDSESEKICTVOVGNSTMPGYPTFOALACQVYMSW	300	
Db	301	DQLPSRALGPAAPLTPLESPPAGSPAMMLAQGPOLYVMDAVPARRMKEFYRTGLREAE	360	
Qy	301	DQLPSRALGPAAPLTPLESPPAGSPAMMLAQGPOLYVMDAVPARRMKEFYRTGLREAE	360	
Db	361	IEAVEVEIGRFDDQYEMLKKRRQQQPGGLGAVYAAALERMGLDCCVEDLRSRLDRGP	417	
Qy	361	IEAVEVEIGRFDDQYEMLKKRRQQQPGGLGAVYAAALERMGLDCCVEDLRSRLDRGP	417	

ID	W95538 standard: Protein; 417 AA.	Score	DB 1;	Length	417;
AC	W95538;				
DT	25-MAR-1999 (first entry)				
DE	Death domain containing receptor polypeptide (DR3).				
KW	Death domain; receptor; DR3-V1; DR3; recombinant.				
OS	Homo sapiens.				
PH	Key				
FT	Peptide				
FT	1. .24				
FT	/note="signal peptide"				
FT	25. .417				
FT	Protein				
FT	/note="mature protein"				
PN	J11000170-A.				
PD	06-JAN-1999.				
PE	12-MAR-1997; 057503.				
PR	06-FEB-1997; US-037341.				
PR	12-MAR-1996; US-013285.				
PR	17-OCT-1996; US-028711.				
PA	(HUMA-) HUMAN GENOME SCI INC.				
PA	(UNMI) UNIV MICHIGAN.				
DR	WPI: 99-124390/11.				
DR	N-PSDB: X00925.				
PT	New death domain containing receptor and recombinant vector -				
PT	optionally comprising leader sequence				
PS	Claim 1; Fig 3; 50pp; Japanese.				
CC	The invention provides nucleotide sequences encoding death domain				
CC	containing receptor polypeptides DR3-V1 and DR3. The DR3-V1 cDNA clone				
CC	is contained in ATCC depositon No. 97456 and the DR3 cDNA clone is				
CC	contained in ATCC depositon No. 97757. Recombinant vectors comprising				
CC	the nucleic acid sequences and optionally the leader sequences are used				
CC	for the recombinant production of the proteins. The present sequence				
CC	represents the amino acid sequence of a death domain containing receptor				
CC	polypeptide (DR3).				
SO	Sequence 417 AA;				
Query Match	100.0%;	Score	3198;	DB 1;	Length 417;
Best Local Similarity	100.0%;	Pred. No.	6,616-300;		
Matches 417;	Conservative	0;	Mismatches	0;	Indels 0;
					Gaps 0;

QY	1	MEQNRRCGAANAALLLVLLVLAGARQSGSTRBPRDCAGDFHKKIGLPCRCGCGPAGHYLKNAP	60
Db	61	CTEPGNGSTCLVCPQDPTFLAMENHNHNSCARCOACQACQASQVALLENCASAVADTRCGCKRG	120
QY	61	CTEPGNGSTCLVCPQDPTFLAMENHNHNSCARCOACQACQASQVALLENCASAVADTRCGCKRG	120
Db	121	MFVEVQVQCVSSSPFCQCPQLDQALGALHRTLLRCSTRDQDCTCLPGFYEHHDGCVSCP	180
QY	121	MFVEVQVQCVSSSPFCQCPQLDQALGALHRTLLRCSTRDQDCTCLPGFYEHHDGCVSCP	180
Db	181	TSTLGCPCERCAAVCGWRQMFQVOLLAGLVPLLLGATLVYTYTYRHQCPHKLPLVTADEAG	240
QY	181	TSTLGCPCERCAAVCGWRQMFQVOLLAGLVPLLLGATLVYTYTYRHQCPHKLPLVTADEAG	240
Db	241	MEALTPPATLHSLPDSASHNTLLAPDSSSEKICVYQLVGNSMTGCFETQDPAIICPPQTTWSM	300
QY	241	MEALTPPATLHSLPDSASHNTLLAPDSSSEKICVYQLVGNSMTGCFETQDPAIICPPQTTWSM	300
Db	301	DQLESRALGPAAPLTLSPESPAGSPAMMLPGPQIYVDMVAPPARMKKEFVRTLGLREAE	360
QY	301	DQLESRALGPAAPLTLSPESPAGSPAMMLPGPQIYVDMVAPPARMKKEFVRTLGLREAE	360
Db	361	TEAVEVEIGFRDDQOYEMLKRWKROQDPAGIGAYTAALERNGLDGCYEDLRSRLQRP	417
QY	361	TEAVEVEIGFRDDQOYEMLKRWKROQDPAGIGAYTAALERNGLDGCYEDLRSRLQRP	417

ID	Accession	Protein Name	Length (AA)
AC	W57045	standard; Protein; 417 AA.	417
DT	20-AUG-1998	(first entry)	
DE	Human apoptosis inducing receptor.		
KM	Apoptosis inducing receptor; AIR protein; human; cell death regulator;		
KW	Type I transmembrane protein; tumour cell death; autoimmune disease;		
KW	therapy.		
OS	Homo sapiens.		
PN	W09814565.A1.		
PD	09-APR-1998.		
PF	03-OCT-1997; U17876.		
PR	04-OCT-1996; U5-044456.		
PA	(IMM) IMMUNEX CORP.		
PI	Perkins PA.		
DR	WPI: 98-240077/21.		
DR	N-PSDB: V28700.		
PT	DNA encoding apoptosis inducing receptor - which is Type I		
PS	transmembrane protein, useful for regulating cell death		
CS	Claim 16: Page 28-30; 45pp; English.		
CC	This sequence is the human apoptosis inducing receptor (AIR) of the		
CC	invention. AIR is a Type I transmembrane protein, soluble forms of which		
CC	can also be used to regulate cell death in a therapeutic setting. Soluble AIR		
CC	can also be used in vitro to block apoptosis or AIR-expressing cells, or		
CC	to screen agonists or antagonists of AIR activity. The cytoplasmic domain		
CC	of AIR can be used to develop assays for inhibitors of AIR-induced cell		
CC	death, which is useful to regulate cell death in a therapeutic setting as		
CC	well as in vitro. Agonists of AIR activity can be used to kill tumour		
CC	cells that express AIR, or T cells expressing AIR in autoimmune diseases		
SQ	Sequence 417 AA;		

Query Match	Score 3198;	DB 1;	Length 417;
Best Local Similarity 100.0%;	Pred. No. 6,61e-300;		
Matches 417; Conservative	0; Mismatches 0;	Indels 0;	Gaps 0;
Db	1	MEORPFGCAVAAALLLVILGARAQGTBPRPRDCADDFHKTKGLFCCRCRGPAGHYLAKP	60
Qy	1	MEORPFGCAVAAALLLVILGARAQGTBPRPRDCADDFHKTKGLFCCRCRGPAGHYLAKP	60
Db	61	CPEPCNSCTLYVPODFTFLAMENHNHNSCARCOACDEQASQVALENCSAAVADTFCGCKPG	120
Qy	61	CPEPCNSCTLYVPODFTFLAMENHNHNSCARCOACDEQASQVALENCSAAVADTFCGCKPG	120
Db	121	WPEVCQVSDCVSSPFYQCPCLDGCALHRTTLLCSRRDTDCGLDPGYEHEDGCYSCP	180

QY 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGCTLPGEYEHGDCVSCP 180  
DB 181 TSTLGSCEPCAAVCGMRFWVYLLAGLVVPLLLGATLTYYTRHCPHPLVTADAEAG 240  
QY 181 TSTLGSCEPCAAVCGMRFWVYLLAGLVVPLLLGATLTYYTRHCPHPLVTADAEAG 240  
DB 241 MEALTTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPTQFALCPQVYMSW 300  
QY 241 MEALTTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPTQFALCPQVYMSW 300  
DB 301 DQPSRALGPAAAPTLPSPSPAGSPAMMLQPGPOLYDVMDAVPARRKEFVRTLGLEBAE 360  
QY 301 DQPSRALGPAAAPTLPSPSPAGSPAMMLQPGPOLYDVMDAVPARRKEFVRTLGLEBAE 360  
DB 361 IEAVEVEIGFRDQOYEMLKRMRQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417  
QY 361 IEAVEVEIGFRDQOYEMLKRMRQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 4  
ID W26709 standard; Protein: 417 AA.  
AC W26709;  
DT 14-APR-1998 (first entry)  
DE Human apoptosis protein Apo-3.  
KW Apo-3; apoptosis; human; therapy.  
OS Homo sapiens.  
FH Key  
FT Peptide  
FT 1..24 Location/Qualifiers  
FT /label= Sig\_peptide  
FT 25..198  
FT Domain  
FT /note= "extracellular domain"  
FT 199..224  
FT /note= "transmembrane domain"  
FT 225..417  
FT Domain  
FT /note= "intracellular domain"  
FT 338..417  
FT /note= "death domain"  
FT Modified\_site 67  
FT /note= "N-glycosylated"  
FT Modified\_site 106  
FT /note= "N-glycosylated"  
FT WO9737020-A1.  
PD 09-OCT-1997.  
PF 31-MAR-1997; U05230.  
PR 23-SEP-1996; US-710802.  
PR 01-APR-1996; US-625328.  
PA (GENE) GENENTECH INC.  
PI Ashkenazi AJ;  
DR WPI: 97-503105/46.  
DR N-PSDB: T91180.  
PT Polypeptide(s) Apo-3 and Apo-2L1 - useful for regulating apoptosis  
PT in mammalian cells  
PS Claim 19; Page 46-48; 70pp; English.  
CC This novel polypeptide, designated Apo-3, is a protein that  
CC stimulates or induces apoptotic activity in mammalian cells  
CC purposes. Its amino acid sequence was deduced from a human foetal  
CC heart cDNA clone (see T91180). The N-terminal 181 amino acids of  
CC Apo-3 are identical to the sequence of another novel apoptosis  
CC polypeptide, Apo-2L1 (see W26709). Also claimed are: polypeptides  
CC comprising the extracellular or death domain of Apo-3; chimeric  
CC molecules comprising Apo-3 fused to a heterologous amino acid  
CC sequence; antibodies that bind to Apo-3 or its extracellular  
CC domain; nucleic acids encoding the polypeptides, as well as  
CC vectors and host cells; a non-human transgenic animal containing  
CC cells that express nucleic acid encoding Apo-3; and a non-human  
CC knockout animal containing cells having an altered Apo-3 gene.  
CC Apo-3 can be used to induce apoptosis or NF-kappa-B (NF-kB) - or  
CC JNK-mediated gene expression for therapeutic purposes. Apo-3-IgG  
CC fusion proteins can be used to inhibit apoptosis or NF-kB  
CC induction or JNK activation for therapeutic purposes, and can  
CC be used as immunogens for anti-Apo-3 antibody production.  
CC Apo-3 or Apo-2L1 can also be used as assay standards. The  
CC animals can be used in drug screening and development.

SO Sequence 417 AA;  
Query Match 100.0%; Score 3198; DB 1; Length 417;  
Best Local Similarity 100.0%; Pred. No. 6,61e-300;  
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MEORRGCAAAVAAALLLVLLGARAGCGTRSPRCOAGDFHKKIGLFCRCGCPAGHYLKAP 60  
QY 1 MEORRGCAAAVAAALLLVLLGARAGCGTRSPRCOAGDFHKKIGLFCRCGCPAGHYLKAP 60  
DB 61 CTEPGNSTCLVCPQDFTFLAMENHNHNSPCARCOACDEQASQVALENCASAVADTRCGCKRG 120  
QY 61 CTEPGNSTCLVCPQDFTFLAMENHNHNSPCARCOACDEQASQVALENCASAVADTRCGCKRG 120  
DB 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGCTLPGEYEHGDCVSCP 180  
QY 121 WFEVQVSGVSSSPFYQPCLDGALHRRHRLRLCSRRDTCGCTLPGEYEHGDCVSCP 180  
DB 181 TSTLGSCEPCAAVCGMRFWVYLLAGLVVPLLLGATLTYYTRHCPHPLVTADAEAG 240  
QY 181 TSTLGSCEPCAAVCGMRFWVYLLAGLVVPLLLGATLTYYTRHCPHPLVTADAEAG 240  
DB 241 MEALTTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPTQFALCPQVYMSW 300  
QY 241 MEALTTPPATHTLSPDLSAHTLLAPPDSSEKICTYQVLGNSMTPGYPTQFALCPQVYMSW 300  
DB 301 DQPSRALGPAAAPTLPSPSPAGSPAMMLQPGPOLYDVMDAVPARRKEFVRTLGLEBAE 360  
QY 301 DQPSRALGPAAAPTLPSPSPAGSPAMMLQPGPOLYDVMDAVPARRKEFVRTLGLEBAE 360  
DB 361 IEAVEVEIGFRDQOYEMLKRMRQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417  
QY 361 IEAVEVEIGFRDQOYEMLKRMRQOPAGLGAVYAALERMGLDGCVEDLRSRLQGRP 417

RESULT 5  
ID W64486 standard; Protein: 833 AA.  
AC W64486;  
DT 20-OCT-1998 (first entry)  
DE Human DR3 protein.  
KW Death domain containing receptor 4; DR4; apoptosis; cancer; inflammation;  
KW agonist; tumour necrosis factor; TNF; ligand; autoimmune disease; DR3;  
KW infection; graft rejection; antagonist; inhibitor; diagnostic.  
OS Homo sapiens.  
PN WO9832856-A1.  
PD 27-JAN-1998; U01464.  
PF 27-JAN-1998;  
PR 05-FEB-1997; US-037829.  
PR 28-JAN-1997; US-035722.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PI (UNMT) UNIV MICHIGAN.  
DR Dixit VM, Gentz RL, Ni J, Pan JG, Rosen CA;  
PT Nucleic acid encoding human death domain-containing receptor 4 -  
PT useful for therapeutic modulation of apoptosis, in e.g. cancer and  
PT autoimmune diseases  
PS Disclosure; Fig 2; 92pp; English.  
CC This sequence represents the human death domain containing receptor-3  
CC DR3 which is used in a method resulting in the isolation of a human death  
CC domain containing receptor 4, DR4. DR4 agonists are used to increase  
CC apoptosis induced by tumour necrosis factor (TNF)-family ligands, e.g. in  
CC cases of cancer, autoimmune disease, viral or other infections,  
CC inflammation, graft vs. host disease, acute or chronic graft rejection.  
CC Antagonists of DR4 are used to inhibit such apoptosis, e.g. in cases of  
CC acquired immune deficiency syndrome, neurodegenerative disease,  
CC myelodysplastic syndrome, ischaemic injury, toxin-induced liver damage,  
CC septic shock, cachexia and anorexia, also a wide range of inflammatory  
CC conditions. DR4 of fragments of the protein are used diagnostically, e.g.  
CC to detect mutant forms of DR4 (possibly associated with disease), for  
CC isolating the DR4 gene or related sequences and for chromosomal mapping.  
SQ Sequence 833 AA;  
Query Match 100.0%; Score 3198; DB 1; Length 833;









Db 435 IEEL 439  
QY 409 LRSRL 413

RESULT 12  
ID R07451 standard; protein; 455 AA.  
AC R07451;  
DT 29-JAN-1991 (first entry)  
DE Human Tumour Necrosis Factor-Receptor from lambdaTNF-R2 cDNA insert.  
KW Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;  
KM Infectious disease; parasitic disease; cachexia;  
KW autoimmune disease; shock; lambdaTNF-R2; ratTNF-R8.  
OS Homo sapiens.  
PN RP-393438-A.  
PD 24-OCT-1990.  
PF 06-APR-1990; 106624.  
PR 21-APR-1989; DE-913101.  
PR 21-JUN-1989; DE-920282.  
PA (BOEH) BOEHRINGER INGELHEIMINT.  
PI Hauptmann R, Himmeler A, Maurer-Fogy I, Stratowa C;  
DR WPI; 90-321987/43.  
DR N-PSDB; Q06285.  
PT DNA encoding TNF binding protein and TNF-receptor - used in  
PT tumour treatment and to understand mechanism to TNF action  
PS Disclosure: Fig 91(1-2); 51pp; German.  
CC ratTNF-R8 (Q06284) was used to screen the HS9137 cDNA library.  
CC lambdaTNF-R2 encodes the complete human TNF-R2 and was used to  
CC construct a plasmid (pADTNF-R) expressing the product the same way  
CC as pADTNF-BF (see Q06282). The expressed proteins are useful  
CC prophylactically and therapeutically to control disorders which  
CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
CC respiratory distress syndrome etc., or side effects of treatment with  
CC TNF-alpha). They can also be used as diagnostic reagents for  
CC assaying TNF and in study of TNF-receptor interactions.  
CC See also Q06282-Q06285.  
SQ Sequence 455 AA:

Query Match 12.8%; Score 408; DB 1; Length 455;  
Best Local Similarity 29.9%; Pred. No. 5.05e-26;  
Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDSCPGKXIIHPONNSICCTCKHKGITLYLNDCCPGQDPTDCRECS 86  
QY 19 LLGARAQGGTRSPR-CDCA-GDF-HKRTGLFCRCGPAGHYLKAPCTEPCGNSGTCVCPQ 75  
Db 87 GSFTASENHLR-HCLSCSKCKREMGQVEISSCTVDRDTCGCRKNQYRHW-SENLFQC- 143  
QY 76 DFLAMENHNHNSCARQACDEQASQVALENCASAVADTRCGCKPGWVEECQVSCVSSSP 135  
Db 144 FNCSLCLN-GTVH---LSCQEKONTVC-TCHAGFFLENECVSCSNCKKSLCTKLCPL 197  
QY 136 FYCQPCDLCGALHRTLRLLC-SRRDTCGTCLPGFYEHGDCVSCPSTIG-SCPERC-A 192  
Db 198 QIONVKGTEDSGTVLLP-LVIFGCLLLSLFLGLMYRQRMKSKLYSIYCKSTPEKE 256  
QY 193 AVCGWRQMF-W-VQVLLAGLV--PL-LLGATLT-YTYR-HCWPHK--PLVTADAE-GME 242  
Db 257 GELEGTTKPLAPNPSFPGFTPLGFSVPVSTSTSSSTVPGDCPNFAARRREYAP 316  
QY 243 A-LTPPATHTLSPLDS-AHTL-LAPDSSSEKICITVOLGNS-WTPGYRPEOALCPQVT- 297  
Db 317 PYGADPITATLASDPIPNPLOKWEDESAHKPOSJTDTPATLYAVVENVPRLRKEFVR 376  
QY 298 -W-SMDQLPSRALGPAAPFT-LSP-ESPAGSPAMMLQPGPO-LYDVMADAVPARRKEFVR 352  
Db 377 RLGLSDHEIDRLQNGRCLEAPQYSLATWRRTTTPREATTLELLGLVLRMDLGLCED 436  
QY 353 TLGLREAEIYEAIVEIGR-FRDOQYEMLKRMROQP--AGLGAVALAERMGIDGVED 408  
Db 437 IEEL 441

QY 409 LRSRL 413

RESULT 13  
ID R10986 standard; protein; 455 AA.  
AC R10986;  
DT 13-MAY-1991 (first entry)  
DE 30kD TNF inhibitor precursor.  
KW Tumour necrosis factor; inhibitor.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT cleavage\_site 40..41  
FT note=" cleavage gives active protein "  
PN AU9058976-A.  
PD 24-JAN-1991.  
PF 16-JUL-1990; 058976.  
PR 18-JUL-1989; US-381080.  
PR 11-DEC-1989; US-450329.  
PR 07-FEB-1990; US-479661.  
PA (SYNE-) SYNERGEN INC.  
DR WPI; 91-073847/11.  
DR N-PSDB; Q10883.  
PT Tumour necrosis factor inhibitor - for suppression of TNF-alpha  
PT and -beta, useful as therapeutic agent.  
PS Disclosure: Fig 21; 142pp; English.  
CC The sequence comprises the entire 30 kD TNF inhibitor. The clone  
CC from which the sequence was deduced was isolated from a cDNA  
CC library prep. from RNA from 0937 cells treated with PMA/PMA.  
CC The whole gene can be inserted into expression vectors for prepn.  
CC of TNF inhibitor for use in the treatment of inflammatory and  
CC degenerative diseases. The active protein is claimed (Claim 8).  
SQ Sequence 455 AA:

Query Match 12.7%; Score 407; DB 1; Length 455;  
Best Local Similarity 29.9%; Pred. No. 6.26e-26;  
Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

Db 27 VIGLVPHLGDREKRDSCPGKXIIHPONNSICCTCKHKGITLYLNDCCPGQDPTDCRECS 86  
QY 19 LLGARAQGGTRSPR-CDCA-GDF-HKRTGLFCRCGPAGHYLKAPCTEPCGNSGTCVCPQ 75  
Db 87 GSFTASENHLR-HCLSCSKCKREMGQVEISSCTVDRDTCGCRKNQYRHW-SENLFQC- 143  
QY 76 DFLAMENHNHNSCARQACDEQASQVALENCASAVADTRCGCKPGWVEECQVSCVSSSP 135  
Db 144 FNCSLCLN-GTVH---LSCQEKONTVC-TCHAGFFLENECVSCSNCKKSLCTKLCPL 197  
QY 136 FYCQPCDLCGALHRTLRLLC-SRRDTCGTCLPGFYEHGDCVSCPSTIG-SCPERC-A 192  
Db 198 QIONVKGTEDSGTVLLP-LVIFGCLLLSLFLGLMYRQRMKSKLYSIYCKSTPEKE 256  
QY 193 AVCGWRQMF-W-VQVLLAGLV--PL-LLGATLT-YTYR-HCWPHK--PLVTADAE-GME 242  
Db 257 GELEGTTKPLAPNPSFPGFTPLGFSVPVSTSTSSSTVPGDCPNFAARRREYAP 316  
QY 243 A-LTPPATHTLSPLDS-AHTL-LAPDSSSEKICITVOLGNS-WTPGYRPEOALCPQVT- 297  
Db 317 PYGADPITATLASDPIPNPLOKWEDESAHKPOSJTDTPATLYAVVENVPRLRKEFVR 376  
QY 298 -W-SMDQLPSRALGPAAPFT-LSP-ESPAGSPAMMLQPGPO-LYDVMADAVPARRKEFVR 352  
Db 377 RLGLSDHEIDRLQNGRCLEAPQYSLATWRRTTTPREATTLELLGLVLRMDLGLCED 436  
QY 353 TLGLREAEIYEAIVEIGR-FRDOQYEMLKRMROQP--AGLGAVALAERMGIDGVED 408  
Db 437 IEEL 441  
QY 409 LRSRL 413  
RESULT 14

ID	R75084 standard; Protein; 455 AA
AC	R75084; (first entry)
DT	19-JAN-1996
DE	p55 TNF-R
KW	p55, tumour necrosis factor receptor; TNF-R; human; murine; chimera;
KW	epidermal growth factor receptor; EGF-R; protease; inhibitor;
XW	phorbol myristate acetate; PMA.
OS	Homo sapiens.
PB	Key
FT	peptide
FT	Location/Qualifiers
FT	41..53
FT	/note= "N terminus of soluble p55 TNF-R"
FT	54..56
FT	/note= "glycosylation site"
FT	145..147
FT	/note= "glycosylation site"
FT	161..163
FT	/note= "glycosylation site"
FT	193..210
FT	/note= "peptide used in creation of chimeras"
FT	198..210
FT	/note= "spacer region"
FT	201
FT	/note= "major C terminus for soluble p55 TNF-R"
FT	202
FT	/note= "essential for shedding reaction"
FT	203
FT	/note= "minor C terminus for soluble p55 TNF-R"
FT	212..234
FT	/note= "transmembrane region"
PN	AU945742-A.
PD	04-MAY-1995.
PR	11-OCT-1994; 075742.
PR	12-OCT-1994; IL-107268.
PA	(YEDA) YEDA RES & DEV CO LTD.
PI	Batkin M, Brakebusch C, Varfolomeev E, Wallach D;
DR	WPI; 95-194342/26.
N-PSDB:	090513.
PT	New protease capable of cleaving soluble tumour necrosis factor
PT	(TNF) receptor . from cell-bound TNF- receptor, useful for
PT	antagonising deleterious effects of TNF.
PS	Disclosure; Fig 1; 40pp; English.
CC	This sequence represents human p55 tumour necrosis factor (TNF-R).
CC	Expression of this receptor is regulated by shedding of the extracellular
CC	receptor fragment. The p55 TNF-R can be shed in response to different
CC	inducing agents, e.g. phorbol myristate acetate (PMA), depending on cell
CC	type. The only region of the receptor whose structure affects the
CC	shedding response is the spacer region (see R75012) in the extracellular
CC	domain. This region is located close to a site of cleavage of the
CC	molecule, and links the Cys rich module to the transmembrane domain. The
CC	spacer region of the encoded protein was used to create the chimeras
CC	between human p55 TNF-R and murine epidermal growth factor receptor
CC	(EGF-R) that are represented by R75007-11. This spacer region was
CC	subjected to deletion mutations (R75013-25) and substitutions
CC	(R75026-47). Of the spacer region, the most important residues are
CC	Asn 172, Val 173, Lys 174 and Gly 175, with Val 173 being the most
CC	important of these. The shedding of the receptor is independent of the
CC	cysteine chain identity of these residues, with the exception of a limited
CC	dependence on the identity of Val 173. Mutations which alter the
CC	conformation of the protein adversely effect the shedding process.
CC	The mutations shown in R75013-47 were introduced in order to create an
CC	inhibitor of a protease that is capable of cleaving the soluble TNF-R
CC	from the cell bound TNF-R. Fragments of these inhibitors can be seen in
CC	R75017-9, R75033-5 and R75042-3. These protease inhibitors can
CC	be used for enhancing TNF function.
SQ	Sequence 455 AA:
Query Match	12.7%; Score 407; DB 1; Length 455;
Best Local Similarity	29.9%; Pred. No. 6.2e-26;
Matches 127; Conservative	81; Mismatches 177; Indels 40; Gaps 32;

Db	87	GSTFASNNHR-HCLSCNCRKEMGOVELISCGVDRDPTVCGCRKNQYHHYV-SENTLFGC-	143
Qy	76	DTFLFAMNHNNSCARQADDEQASVALENCSNAVDTRCGCKPPMPFVECVQSSCVSSP	135
Db	144	FNSICLHN-GTVH----LSCQEKONTVC-TCHAGFFLRENECVSCSNCKSLSECTKLC	197
Qy	136	FYCGPCDGCALHRRHRLILC-SRRDPTDCGNCILPGFEHGDGVCPTSLTG-SCPERC-A	192
Db	198	QIENKCTEDSGTTVLLP-LVIFFGCLLSLFIIGLMTYQVQWKKSKIKSIYCGKSTPEKE	256
Qy	193	AVCGWRQMF-W-VQVLLAGLVV--PL-LLGATLLT-YTRY-HCWPKR--PLVYADDA-GME	242
Db	257	GELEGTTRKPLAIVNPSPSPPTPLGFSFVSSSTFTSSSTYTPGDGCNFAAPREYAP	316
Qy	243	A-LTPPATHLSPDS-AHTL-LAPDSSBKICTQVLVANS-WTGYCPETGALCPQYT-	297
Db	317	PYQAGDPIIATALASDIPNPLOKWEDESAHKPOSUDTDPAFLIYAVENVAPPLRKEEYR	376
Qy	298	-W-SMDQPLPRALGPAAAPL-LSP-ESPAGSPMMILOPPO-LYDVAVAPARRKKEEYR	352
Db	377	RLGISDEIDRIELQNGRCIREAQVSMLATWRRRTPREATTLELGRVLRDDLLGCELD	436
Qy	353	TVLGREAEIEAVEVEIGR-FRDOQYEMLRKWRQOP--AGIGAVYALERNGLDGCEVD	408
Db	437	IEEAL 441	
Qy	409	LRSRL 413	
RESULT	15		
ID	R42059	standard; Protein; 455 AA.	
AC	R42059;		
DT	29-APR-1994	(first entry)	
DE	Lambda derived TNF-R.		
KW	Human; tumour necrosis factor receptor; TNF-R; interleukin-1 receptor		
KW	IL-1R; fusion protein; linker; TNF; IL-1; cachexia; cerebral malaria;		
KW	rheumatoid arthritis; diabetes; multiple sclerosis; septic shock;		
KW	pulmonary fibrosis; silicosis; allograft; xenograft; rejection;		
KW	griif verses host disease; sepsis; inflammation; allergy;		
KW	autoimmune dysfunction.		
OS	Homo sapiens.		
OS	Lambda.gli0-7ctnfbp.		
FH	Key	Location/Qualifiers	
FT	peptide	1..40	
FT	protein	41..455	
FT		/note="Signal peptide"	
FT		/note="Mature hTNF-R"	
PN	W09319777-A.		
PD	14-OCT-1993.		
PF	26-MAR-1993; U02938.		
PR	30-MAY-1992; U5-860710.		
PA	(IMMV ) IMMUNEX CORP.		
PI	Smith CA;		
PI	WPI: 93-336592/42.		
DR	N-PSDB; 049932.		
PT	New fusion protein tumour necrosis factor and human interleukin-1		
PT	receptor - useful in therapy, diagnosis and assays of e.g.		
PT	rheumatoid arthritis, diabetes, cerebral malaria, sepsis, etc.		
PS	Disclosure: Page 57-59; 85pp; English.		
CC	The sequences given in R42058-59 represent human tumour necrosis		
CC	factor receptor (TNF-R) and the sequences in R42060-61 represent		
CC	human interleukin-1 receptor (IL-1R). These sequences were used in		
CC	the production of a fusion protein which conformed to one of the		
CC	formulae:		
CC	TNF-R-linker-TNF-R-linker-IL-1R		
CC	IL-1R-linker-TNF-R-linker-TNF-R or		
CC	TNF-R-linker-TNF-R		
CC	The linker may comprise 5-100 amino acids selected from Gly, Asp,		
CC	Ser, Thr and Ala. These linkers separate the individual moieties		
CC	by such a distance that each component of the fusion protein is		
CC	capable of folding into the secondary or tertiary structure required		
CC	for its biological activity. These fusion proteins may be used in		

CC therapy, diagnosis and assays for conditions mediated by TNF or IL-1,  
CC particularly in conditions in which both TNF and IL-1 play a causative  
CC role. They may be used to treat cachexia, rheumatoid arthritis,  
CC diabetes, multiple sclerosis, pulmonary fibrosis and silicosis,  
CC cerebral malaria, allograft and xenograft rejection in graft verses  
CC host disease, sepsis, septic shock, inflammation, allergies and  
CC autoimmune dysfunctions.  
SQ Sequence 455 AA;

Query Match 12.7%; Score 407; DB 1; Length 455;

Best Local Similarity 29.9%; Pred. No. 6.26e-26;

Matches 127; Conservative 81; Mismatches 177; Indels 40; Gaps 32;

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Db 27 VIGLPHLDREKRDVCPQGYIHPONNSICCTKCHKGYLNDPCPGQDTRCECES 86
OY 19 LIGARAQGGTRSPR-CDCA-GDF-HKKIGLFCRCGPACHYLLKAPCTEPCGNSTCLVCPQ 75
Db 87 GSFTASENHLR-HCLSCSKCRKEMGOVEISSCTVDRDTVCGCRKNQRYHYW-SENLFQC- 143
OY 76 DTFLEAMENHNSECARCQACDEQASQVLENCASAVADTRCGCKPGMFVEQVSCVSSSP 135
Db 144 FMSCLCN-GTVH---LSCQEKQNTVC-TCHAGFPLRENECVSGSNCKKSLECTKLCUP 197
OY 136 FYCQPCLDGALHRTLRILC-SRRTDCCGTCLEGFYEHGDCVSCPTSLG-SCPERC-A 192
Db 198 OIENKGTEDSGTYLLP-LVTFPGICLISLFIGLMRYQRMKSKLYSTVCGSKSTEPEK 256
OY 193 AVCGWRQMF-W-VQVLLAGLV--PL-LIGATLT-YTYR-HCPMK--PLVTADCA-GME 242
Db 257 GELEGTTKPLAPNPSFPTPGFTPLGFSVPSSSTFTSSSTYTPGDCPNFAAPRRVAP 316
OY 243 A-LTPPPATHLSPLDS-AHTL-LAPPDSSSEKICTVQVGNLS-WTPGYPETQEAICPQVT- 297
Db 317 PYGADPILATLASDPIFNPLQKWEDESAHKFQSLDTPDPAITYAVENVPLRMKEFYR 376
OY 298 -W-SWDQLPSRAIGPAAAPT-LSP-ESPAGSPAMMLQPGPO-LYDVMDAVPARRMKEFYR 352
Db 377 RLGLSDHEIDRLONGRCLREAOYSMLATWRRRTPRREATLELGLRVLRDMDLGCLLD 436
OY 353 TLGLREAEIEAVEVEIGR-FRDOYEMLRKMQOP--AGLGAVYALERMGLDGCVED 408
Db 437 IEAL 441
OY 409 ILSRL 413
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